

וְעַמְקָדָן

RESULT 1	BUT59674/c	BUT59674	616 bp	mRNA	linear	EST 10-OCT-2002
LOCUS	6574	UI-R-FFO-cpf-c-16-0-UI	s1	UI-R-FFO	Rattus norvegicus	cDNA clone
DEFINITION		UI-R-FFO-cpf-c-16-0-UI 3'				, mRNA sequence.
ACCESSION	BUT59674	BUT59674				
VERSIONS	1	BUT59674.1	GI : 23123459			
KEYWORDS		EST				
SOURCE		Rattus norvegicus	(Norway rat)			
ORGANISM		Rattus norvegicus				
		Pearson et al., 1999				
		Chordata				
		Gnathostomata				
		Vertebrata				
		Euteleostomi				

Result	Score	Query Length	DB ID	Description
28: gb_gss1:*				
29: gb_gss2:*				
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.				
				SUMMARIES
				%

issue Procurement: Jeff Stevens, University of Iowa
 cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
 cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 cDNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 cDNA Distribution: DISTRIBUTION: Researchers may obtain clones
 from Research Genetics (www.resgen.com).
 The following repetitive elements were found in this cDNA
 sequence: 1-26, >POLY_A\$imile_repeat (matched compliment)
 eq. primer: M13 FORWARD
 OLI4=Yes.

Location/Qualifiers

1.. 616

/organism="Rattus norvegicus"
/mol type="mRNA"
/db_xref="mRNA:10116"
/clone="UI-R-RFFO-1cpf-c-16-0-UI"
/tissue type="Mixed tissues"
/dev stage="Adult"
/lab="DHBIO (Life Technologies) (T1 phage resistant)"
/clone_id="UI-R-RFFO"
/note="Vector: pT7T3-Pac (Pharmacia) with a modified
polylinker; Site 1: EcoRI I; Site 2: Not I; UI-RFFO is a
subtracted cDNA library containing the following
tissues: Normal cartilage and SR-JWS Tumor Line. The
subtraction was made according to Bonaldo, Lennon and
Soares, Genome Research, 6:791-806, 1996. The
oligonucleotide used to prime the synthesis of
first strand cDNA contains a library tag sequence that is
located between the Not I site and the (dtr)18 tail. The
sequence tags for these libraries are: CTATGGACG,
CATTCCTCTGA,
TAG_TISSUE=cartilage
TAG_LIB=UI-R-RFFO

IGIN					
TAG_SEQ=CTAATGGACG"					
Query	Match	Score	DB	Length	
Best Local Matches	94.3%	449	13	616;	
Similarity	99.0%	Pred. No.	1..1e-11;		
Conservative	99.0%	0;	Mismatches	3;	
Matches	473;	Indels	2;	Gap	
1	ATGCTGCCATGAAGCTTCACTGCTCTTGACGGCTTAGCTGGTTGGCTGTGCA				
558	ATGCTGCCATGAAGCTTCACTGCTCTTGACGGCTTAGCTGGTTGGCTGTGCA				
61	T-CCAGGGGCCCTGTCGTGGAAACAACTCAAAGAAATGGAGTGTGCCTTC				
498	TCCCCAGGGGCCCTGTCGTGGAAACAACTCAAAGAAATGGAGTGTGCCTTC				
120	TGAAGTGTGGCCGAGACTGCGGCCATGGAACTGTGCTTAATTGAGATGATC				
438	TGAAGTGTGGCCGAGACTGCGGCCATGGAACTGTGCTTAATTGAGATGATC				
180	ACACCTTAATGAAGTGTCTCATATAATTCACTGGCTCATGTCCTCTGAGTCGCTGT				
378	ACACCTTAATGAAGTGTCTCATATAATTCACTGGCTCATGTCCTCTGAGTCGCTGT				
240	TGGCTGCTGTGTGACGGGTCTGACGAGGTCTGACGCTGTGGCTTAAGACAGCACATCACT				
318	TGGCTGCTGTGTGACGGGTCTGACGAGGTCTGACGCTGTGGCTTAAGACAGCACATCACT				
300	GCGATCTTAAGATCCCTAACGGCTTACGGATCTGAGCAATCTTACGGATCTGAGCACTTC				
258	GCGATCTTAAGATCCCTAACGGCTTACGGATCTGAGCAATCTTACGGATCTGAGCACTTC				
360	TCAAGGATGACTCTGGAAATGGAGGGCTATTCTGGAGAGCAAAAGGCAGAAAGGAGG				
198	TCAAGGATGCTGGAAATGGAGGGCTATTCTGGAGAGCAAAAGGCAGAAAGGAGG				
420	AACCAAGGGAAAGACGAAAGCAGAAACCCAGAACGACTGGAGAACCCACCTGTGA				
138	AACCAAGGGAAAGACGAAAGCAGAAACCCACCTGTGA				

RESULT	2
CB797697	CB797697
LOCUS	AMGNNUC:MRPE4-00164-G5-A
DEFINITION	mRNA (10380) Rattus norvegicus cDNA clone
ACCESSION	mrpe4-00164-95
VERSION	5'
KEYWORDS	mRNA sequence.
SOURCE	Rattus norvegicus (Norway rat)
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Ruteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
RATTUS	Rattus.
REFERENCE	1 (bases 1 to 421)
AUTHORS	Amgen EST Program.
TITLE	Amgen Rat EST Program
JOURNAL	Unpublished (2003).
COMMENT	Contact: Dan Fitzpatrick Amgen, Inc One Amgen Center Drive, Thousand Oaks, CA 91320-1799, USA Tel: 805-447-4881
FEATURES	Plate: 00164 row: 9 column: 5. Location/Qualifiers
source	1. .421 /organism="Rattus norvegicus" /mol_type="mRNA" /db_xref="" /taxon:10116" /clone:"mrpe4-00164-95" /tissue_type="placenta embryo" /clone_idb="mrpe4 (10380)" /note="Infect: pSPRT01; Site_1: Sall; Site_2: NotI; placenta embryo day 17"

Query	Match	Score	419-4;	DB	14;	Length	421;
		Best Local Similarity	99.8%	Pred. No.	2.5e-105;		
		Matches	420;	Mismatches	0;	Gaps	0;
Y	Y	3	GCTGGCCATGAAAGCTGTCACTTGCTTCTGAGGTCTAGCTGGGTGGCTGTGCACTC	62			
Y	Y	1	GCTGGCCATGAAAGCTGTCACTTGCTTCTGAGGTCTAGCTGGGTGGCTGTGCACTC	60			
Y	Y	63	CCAGGGGGCCCTGCTGGAAACAACTCAAAGAAATGGAAGTGGTGCCTTCATAATGA	122			
Y	Y	61	CCAGGGGGCCCTGCTGGAAACAACTCAAAGAAATGGAAGTGGTGCCTTCATAATGA	120			
Y	Y	123	AGTGTGGGGCGGCACTACTGGCGGCAATTGGAGAAGCTGGAGACTGGTGTACATTGCA	182			
Y	Y	121	AGTGTGGGGCGGCACTACTGGCGGCAATTGGAGAAGCTGGTGTACATTGCA	180			
Y	Y	183	CCCTTAATGAGTGTCTCATATAATTCAAGTCCGTCATGNGTCCTTCTGAGTCG	242			
Y	Y	181	CCCTTAATGAGTGTCTCATATAATTCAAGTCCGTCATGNGTCCTTCTGAGTCG	240			
Y	Y	243	CTGCTGTGGTGAAGGGGTCTGCACTGTGTGCGCAATTGGAGAAGCCAAACATCA	302			
Y	Y	241	CTGCTGTGGTGAAGGGGTCTGCACTGTGTGCGCAATTGGAGAAGCCAAACATCA	300			
Y	Y	303	GATCTTAAGATTCCCCCAATCGGGATCCACATTCCACCTGGAGATGACATTCTCTCA	362			
Y	Y	301	GATCTTAAGATTCCCCCAATCGGGATCCACATTCCACCTGGAGATGACATTCTCTCA	360			
Y	Y	363	GGATGTACTTGCGATGCGGGCTTATCTGAGAGACAAGGCAAAAGGAAAC	422			
Y	Y	361	GGATGTACTTGCGATGCGGGCTTATCTGAGAGACAAGGCAAAAGGAAAC	420			
	/	423	C	423			
	/	421	C	421			

Db	346	GAAGTGTGGGTGCGGGTACTGTGGGCCATGGAAAGCTGGTACATCTGGATGAA	405	JOURNAL REFERENCE AUTHORS	Nature 420, 563-573 (2002) 6 (bases 1 to 1583)
Qy	181	CACCCATAAGTCAATTCTCATATTCAGTCATCCGTCATGTCCTCTGAGTCGTGACT	240	Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W., Hayashi,D., Hayatsu,M., Hiramoto,R., Hiroaka,T., Hiroane,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Itoh,T., Kasukawa,T., Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Komoc,H., Kouda,M., Nakamura,M., Nishii,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Shiba,T., Shirakawa,A., Shirakai,T., Shirakawa,A., Sogabe,Y., Tagami,D., Tagami,M., Tachibana,A., Takahashi,F., Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A., Muramatsu,M., and Hayashizaki,Y.	
Db	406	TACCTGTATGAGGTGTCACATTCAGTCGTTGCTGAGTCGTGTTGACT	465	TITLE JOURNAL	Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel: +81-45-503-9222, Fax: +81-45-503-9216)
Qy	241	GCGTGCTGTGGTGAAGGAGCTGACTCTGTGCCTAAAGACCAAACATCACTATG	300	CDNA 1 library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in RIKEN. Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.	
Db	466	GGCTGCTGTGGTGAAGGACCAACATCACTATG	525	COMMENT	Please visit our web site for further details. URL:http://fantom.gsc.riken.go.jp/
Qy	301	CAGATCTTAAGATCCTCCCAATCGGATCCACATTCTACGTGGAGATGACATTCT	360	FEATURES source	CDNA 1 library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in RIKEN. Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Db	526	CAGATCTTAAGATCCTCCCAATCGGATCCACATTCTATGTGGAGATGACATTCT	585	COMMENT	CDNA 1 library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in RIKEN. Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Qy	361	CAGGATGTAATCTGGATGTCGGCTATTCGGAGACGACAAGGGAAAGGGAAA	420	COMMENT	CDNA 1 library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in RIKEN. Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Db	586	CAGGATGTAATCTGGATGTCGGCTATTCGGAGACGACAAGGGAAAGGGAAA	645	COMMENT	CDNA 1 library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in RIKEN. Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Qy	421	ACCAAGGGAGAGGAAAGGAAAGAACCAACCCAGATCTGAGAACCCACCTGTGA	477	FEATURES source	CDNA 1 library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in RIKEN. Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Db	646	ACCAAGGGAGAGGAAAGGAGATGAACTCACAGCTGAGAACCCACCCGTGA	702	COMMENT	CDNA 1 library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in RIKEN. Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
RESULT	5			COMMENT	CDNA 1 library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in RIKEN. Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
ACCESSION	AK042891	AK042891	1583 bp mRNA linear	COMMENT	CDNA 1 library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in RIKEN. Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
DEFINITION		Mus musculus 7 days neonate cerebellum cDNA, RIKEN full-length enriched library, clone: A730035M09 product: placental growth factor, full insert sequence.		COMMENT	CDNA 1 library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in RIKEN. Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
VERSION		AK042891	1	COMMENT	CDNA 1 library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in RIKEN. Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
KEYWORDS		HTC; CAP trapper		COMMENT	CDNA 1 library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in RIKEN. Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
SOURCE		Mus musculus (house mouse)		COMMENT	CDNA 1 library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in RIKEN. Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
ORGANISM		Mus musculus		COMMENT	CDNA 1 library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in RIKEN. Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
REFERENCE		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognath; Muridae; Murinae; Mus.		COMMENT	CDNA 1 library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in RIKEN. Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
AUTHORS		Carninci,P. and Hayashizaki,Y.		COMMENT	CDNA 1 library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in RIKEN. Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
TITLE		High-efficiency full-length cDNA cloning		COMMENT	CDNA 1 library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in RIKEN. Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
JOURNAL		Meth. Enzymol. 303, 19-44 (1999)		COMMENT	CDNA 1 library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in RIKEN. Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
PUBLMED		10349336		COMMENT	CDNA 1 library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in RIKEN. Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
REFERENCE		Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.		COMMENT	CDNA 1 library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in RIKEN. Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
AUTHORS		Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes		COMMENT	CDNA 1 library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in RIKEN. Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
JOURNAL		Genome Res. 10 (10), 1617-1630 (2000)		COMMENT	CDNA 1 library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in RIKEN. Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
PUBLMED		1049374		COMMENT	CDNA 1 library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in RIKEN. Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
REFERENCE		Shibata,K., Itoh,M., Aizawa,K., Nagioka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Harama,M., Nishime,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watanuki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsushita,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kiris,A., and Hayashizaki,Y.		COMMENT	CDNA 1 library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in RIKEN. Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
AUTHORS		RIKEN integrated sequencing pipeline with 384 multicapillary sequencer		COMMENT	CDNA 1 library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in RIKEN. Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
JOURNAL		Genome Res. 10 (11), 1757-1771 (2000)		COMMENT	CDNA 1 library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in RIKEN. Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
PUBLMED		11076861		COMMENT	CDNA 1 library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in RIKEN. Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
REFERENCE		The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.		COMMENT	CDNA 1 library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in RIKEN. Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
AUTHORS		Functional annotation of a full-length mouse cDNA collection		COMMENT	CDNA 1 library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in RIKEN. Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
JOURNAL		Nature 409, 685-690 (2001)		COMMENT	CDNA 1 library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in RIKEN. Genomic Sciences Center and Genome Science Laboratory in Riken contributed to prepare mouse tissues.
AUTHORS		The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.		COMMENT	CDNA 1 library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in RIKEN. Genomic Sciences Center and Genome Science Laboratory in Riken contributed to prepare mouse tissues.
JOURNAL		Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs		COMMENT	CDNA 1 library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in RIKEN. Genomic Sciences Center and Genome Science Laboratory in Riken contributed to prepare mouse tissues.

Db	455	GAACTGGGGTGGAGGTGACTCTGGGCCATGGAGAGCTGGTGTACATTGGATGAA	514	Query Match 86.5%; Score 412.8; DB 12; Length 936;
Qy	181	CACCCCTAATGAGTTGTCATATAATTCACTGTCATGTCCTCTGAGTCCTGTAGT	240	Best Local Similarity 92.2%; Pred. No. 2..3e-103; Gaps 0;
Db	515	TACCTGTATGAGGTGTCATATTCACTGTCCTCTGAGTCCTGTAGT	574	Matches 435; Conservative 0; Mismatches 37; Indels 0; Gaps 0;
Qy	241	GGCTGCTGTGTAACAGGGTCTGCACTGTTGGCCTAAAGACAGCCAACATCATG	300	Qy 1 ATGGTGGCCATGAGGTGTTCACTTGCTCTGGGCTTAGCTGGTTGGCTGTGAC 60
Db	575	GGCTGCTGTGTAACAGGGTCTGCACTGTTGGCCTAAAGACAGCCAACATCATG	634	Db 304 ATGGTGGCCATGAGGTGTTCACTTGCTCTGGGCTTAGCTGGTTGGCTGTGAC 60
Qy	301	CAGATCTAAAGTTCCCCAATCGGATCACATTCACTGGAGATGACATTCT	360	Qy 61 TCCAGGGGGCCCTGTGCTGGAAACACTAACAGAAATGGAGAGCTGGTGTACCTTCACT 120
Db	635	CAGATCTAAAGTTCCCCAATCGGATCACATTCACTGGAGATGACATTCT	694	Db 364 TCCAGGGGGCCCTGTGCTGGAAACACTAACAGAAATGGAGAGCTGGTGTACCTTCACT 423
Qy	361	CAGATGTACTCTCGGAATGCAAGGGCTATTCTGGAGACAAAGGGAAA	420	Qy 121 CAGATGTGGGGCGCAACTGCGGCCAATGGAGAGCTGGTGTACATTGGAGATGAA 180
Db	695	CAGATGTACTCTCGGAATGCAAGGGCTATTCTGGAGACAAAGGGAAA	754	Db 424 GAAGTGTGGGGTGCAGTACTCTGGCCCATGGAGAGCTGGTGTACATGGATGAA 483
Qy	421	ACCAAGGGAAAGGAAAGCAAAACCCCAACCTGTGA	477	Qy 181 CACCTTAATGAGTGTCTCATATTATTCAGTCCTCATGTCCTGAGTCCTGTAGT 240
Db	795	ACCAAGGGAAAGGAAAGCAAAAGGAAAGCTAGGAACTCACTGAGTGTGA	811	Db 484 TACCTGTAGGGTGTCTCACATATTAGTCCTCCATGTCGTGCTGTAGT 543
Qy	RESULT 6			Qy 241 GGCTGCTGGGGTGCAGTACTCTGGCCCATGGAGAGCTGGTGTACATGGATGAA 300
LOCUS	B1905649	936 bp mRNA linear EST 16-OCT-2001		Db 544 GGCTGCTGGGGTGCAGTACTCTGGCCCATGGAGAGCTGGTGTACATGGATGAA 603
DEFINITION	603167660f1 NCI CGAP Lu33 Mus musculus cDNA clone IMAGE:5255846 5', mRNA sequence.			Qy 301 CAGATCTAAAGATTCCCCAACATGGATCCACATTCAGTCCTGAGATGACATTCTCT 360
ACCESSION	B1905649			Db 604 CAGATCTAAAGATTCCCCAACATGGATCCACATTCAGTCCTGAGATGACATTCTCT 663
VERSION	B1905649.1			Qy 361 CAGATGACTCTGGAAATGCAAGCCATTCTGGAGACACAAAGGAGAAA 420
KEYWORDS	EST.			Db 664 CAGATGACTCTGGAAATGCAAGCCATTCTGGAGACACAAAGGAGAAA 723
SOURCE	Mus musculus (house mouse)			
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
REFERENCE	NIH-MSC http://mgc.ncbi.nlm.nih.gov/			Qy 421 ACCAGGGAAAGGAAAGCAAAACCCACCCACCCACC 472
AUTHORS	(bases 1 to 936)			Db 724 ACCAGGGAAAGGAAAGGACGAGGACTGAAACTCACAGACTGAGAACCCAAAC 775
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)			
JOURNAL				
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgapps-r@mail.nih.gov		RESULT 7	
	Tissue Procurement: Gilbert Smith, Ph.D.		AK088943 1579 bp mRNA linear HTC 20-SEP-2003	
	CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D.		LOCUS AK088943	
	CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)		DEFINITION Mus musculus 2 days neonate thymus thymic cells cDNA, RIKEN full-length enriched library, clone E430032N09 product:placental growth factor, full insert sequence.	
	DNA Sequencing by: Incyte Genomics, Inc.		ACCESSION AK088943	
	Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: http://image.llnl.gov		VERSION AK088943.1 GI:26105001	
	Plate: LLAM1646 row: 9 column: 15		KEYWORDS HTC; CAP trapper.	
	High quality sequence start: 9		SOURCE Mus musculus (house mouse)	
	Location/Qualifiers		ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
	1..936 /organism="Mus musculus" 'mol_type="mRNA" 'strain="Czech II"		REFERENCE Carninci, P. and Hayashizaki, Y.	
	/db_xref="taxon:10090" 'clione="IMAGE:5255846" 'tissue type="pooled lung tumors" 'lab host="DRI0B (phage-resistant)" 'clone lib="NCI-CGAP Lu33" 'note="Organ: lung; vector: pRTTD-Pac (Pharmacia) with a modified polylinker; Site 1: NotI; Site 2: EcoRI; 1st strand cDNA was prepared from mRNA obtained from pooled lung tumors with a Not I - oligo (dT) primer [5'-TCATACCATCTGAGTGGAGCCGCCGCTCTGCTTCTTCTTCTT 3']. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pRTTD vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo."	AUTHORS Carninci, P., Shibata, Y., Hayatsu, N., Sugihara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.		
			TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes	
			JOURNAL Genome Res. 10 (10), 1617-1630 (2000)	
			MEDLINE 10349636	
			PUBMED 1104253	
			REFERENCE Carninci, P., Shibata, Y., Hayatsu, N., Sugihara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.	
			AUTHORS Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, S., Ikegami, T., Kashiwagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watanuki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsunaga, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.	
				ORIGIN

TITLE	RICKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
JOURNAL	Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE	20530913
PUBLMED	11073861
AUTHORS	4 The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.
JOURNAL	Functional annotation of a full-length mouse cDNA collection
MEDLINE	Nature 409, 685-690 (2001)
PUBLMED	11073861
AUTHORS	5 The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
JOURNAL	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
MEDLINE	Nature 420, 563-573 (2002)
PUBLMED	11073861
AUTHORS	6 (bases 1 to 1579)
JOURNAL	Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,J., Fukuda,S., Furuno,M., Haragaki,T., Hara,A., Hashizume,W., Hayashizaki,Y., Hayatsu,K., Hirao,T., Hiraoaka,T., Hirorane,T., Horii,F., Imotai,K., Ishii,Y., Itoh,M., Kagawa,I., Kasai,K., Kawai,T., Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Komio,H., Kouada,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Shibata,A., Shinagawa,A., Shiraku,T., Sogabe,Y., Tagami,M., Tagawa,A., Takanashi,F., Takaiwa-Akhirira,S., Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A., Yamamoto,M., and Hayashizaki,Y.
PUBLMED	11073861
AUTHORS	Direct Submission
JOURNAL	Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama 230-0045, Japan (E-mail: genome-res@gsc.riken.go.jp, URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)
MEDLINE	CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in RIKEN Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
PUBLMED	Tissues were provided by Dr. John Todd (Dept. of Medical Genetics Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome Trust/MRC Building Addenbrookes Hospital Cambridge) whose assistance we gratefully acknowledge.
JOURNAL	Please visit our web site for further details.
MEDLINE	URL: http://genome.gsc.riken.go.jp/
PUBLMED	URL: http://fantom.gsc.riken.go.jp/.
AUTHORS	Location/Qualifiers
SOURCE	1. 1.1579 /organism="Mus musculus" /mol_type="mRNA" /strain="NOD" /db_xref="FANTOM_DB:E430032N09" /db_xref="MGI:124_27840" /db_xref="Taxon:10090" /clone="EA3_032N09" /cell_type="thymic cells" /tissue_type="thympus" /clone_id="RIKEN full-length enriched mouse cDNA library putative" 335 . 810 /note="placental growth factor (MGI:105095, GB NM_008827, evidence: BLASTN, 100%, match=1564) 1559 . 1564 /note="paratetic" 1579 /note="putative"
FEATURE	misc_feature
SOURCE	polyA_signal polyA_site
ORIGIN	Query Match

Normalized full-length enriched library from pooled mouse embryonic limb, maxilla and mandible, day 12.5, 13.5, 14.5, and 15.5 (size selected for the 0.5-1 kb fragments) Cloned directionally, priming method: Oligo-dT. cDNA enrichment: >1k bp, Average insert size: 1.6k bp. Normalization (Cot value): 7.5 kb. Priming sequence: 5'-GACTAGTCATGATGCGAGCGGCC(T)³. Tissue contributed by, David Rowe. Library constructed by ResGen, Invitrogen Corp. "

ORIGIN

Query Match 84.9%; Score 405.2; DB 14; Length 932;
Best Local Similarity 91.8%; Pred. No. 2.9e-101;
Matches 439; Conservative 0; Mismatches 38; Indels 1; Gaps 1;

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Db 350 ATGGTGGCATGAGGCTTCAATTGCTCTTCAGGCTCTAGTGTTGGTGTGCA 409

Qy 61 TCCAGGGGCCCCGTCTCTGGAAACAACTAACAGAAATGGAAGTGGCTTCAAT 120
Db 410 TCCAGGGGCCCCGTCTCTGGAAACAACTAACAGAAATGGAAGTGGCTTCAAC 469

Qy 121 GAAGTGTGGGCCAGCTATACTGCGGCCAATGGAAAGCTGGGTACATGGAGATGA 180
Db 470 GAAGTGTGGGTCCAGTACTGTGGCCATGGAAAGCTGGTACATCTGGTGTGAA 529

Qy 181 CACCTTAATGAGTGTCTCATATATTCACTCCCTCATGTCAGTCGCTGTGAGT 240
Db 530 TACCTGTAGGGTGTCTCACATATTCACTCCCTCATGTCAGTCGCTGTGAGT 589

Qy 241 GGCTGTGTGTGTGAGCAGGGTGTGCACTGTGGCCATAAGACAGCCAACTACTATG 300
Db 590 GGCTGTGTGTGTGAGCAGGGTGTGCACTGTGGCCATAAGACAGCCAACTACTATG 649

Qy 301 CAGATCTTAAGATTCCTCCCAATGGGATCCACATTCTACCTGGAGATGACATTCT 360
Db 650 CAGATCTTAAGATTCCTCCCAATGGGATCCACATTCTACCTGGAGATGACATTCT 709

Qy 361 CAGATGTACTCTCGGAAGCAGGCCTATTCTGGAGACAAAGGCAAGAGGAAA 420
Db 710 CAGATGTGTCTGTGAATCAGACCTATTCTGGAGACAAAGGCAAGAGGAAA 769

Qy 421 ACCAA-GGGAAAGGAAAGAAAACCCACAGCTGAGAACCCCACCTGTGA 477
Db 770 ACCAAGGGAAAGGAAAGGGAGGTAGAAACTCACAGACTGAGAACCCCACCTGTGA 827

RESULT 9
LOCUS B0936933 933 bp mRNA linear EST 21-AUG-2002
DEFINITION AGENCOURT 1.0011764 NCI_CGAP_Mam2 Mus musculus cDNA clone IMAGE:6486814 5'_mRNA sequence.
REFERENCE 1 (bases 1 to 933)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC Clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: http://image.llnl.gov

Plate: LIAMI14030 row: m column: 23
High quality sequence stop: 691.
Location/Qualifiers 1..933
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/mol type="mRNA"
/strain="FVB/N-3"
/db_xref="Utraxon:10090"
/clone="IMAGE:6486814"
/tissue type="tumor biopsy sample"
/dev stage="5 months"
/lab host="DH10B"

/clone lib=NCI CGAP Mam2"
/note="Organ: mammary; Vector: pCMV-SPORT6; Site: 1; Sali"
Site: 2; NotI; Cloned unidirectionally; Primer: Oligo dT.
Library constructed by Life Technologies. Investigator providing samples: Gilbert Smith, NIH"

FEATURES source

ORIGIN

	Query Match	Score	Length
	Best Local Similarity	94.9%	933
	Matches	439	
	Conservative	0	
	Mismatches	38	
	Indels	1	
	Gaps	1	
	Score	405.2	DB 13;
	Pred. No.	2.9e-101	
	Mismatches	38	
	Indels	1	
	Gaps	1	

Query Match 84.9%; Score 405.2; DB 13; Length 933;
Best Local Similarity 91.8%; Pred. No. 2.9e-101;
Matches 439; Conservative 0; Mismatches 38; Indels 1; Gaps 1;

Qy 1 ATGGTGGCATGAGGCTTCAATTGCTCTTCAGGCTCTAGCTGGTGTGCA 60
Db 317 ATGGTGGCATGAGGCTTCAATTGCTCTTCAGGCTCTAGTGTTGGTGTGCA 376

Qy 61 TCCAGGGGCCCCGTCTCTGGAAACAACTAACAGAAATGGAAGTGGCTTCAAT 120
Db 377 TCCAGGGGCCCCGTCTCTGGAAACAACTAACAGAAATGGAAGTGGCTTCAAC 436

Qy 121 GAAGTGTGGGCCAGCTACTGGCCATAATGGAAAGCTGGGTACATGGAGATGA 180
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Qy 61 TCCAGGGGCCCCGTCTCTGGAAACAACTAACAGAAATGGAAGTGGCTTCAAT 120
Db 377 TCCAGGGGCCCCGTCTCTGGAAACAACTAACAGAAATGGAAGTGGCTTCAAC 436

Qy 121 GAAGTGTGGGCCAGCTACTGGCCATAATGGAAAGCTGGGTACATGGAGATGA 180
Db 317 GAAGTGTGGGCCAGCTACTGGCCATAATGGAAAGCTGGGTACATGGAGATGA 120

Qy 181 CACCTTAATGAGTGTCTCATATATTCACTCCCTCATGTCAGTCGCTGTGAGT 240
Db 377 TACCTGTAGGGTGTCTCACATATTCACTCCCTCATGTCAGTCGCTGTGAGT 589

Qy 241 GGCTGTGTGTGTGAGCAGGGTGTGCACTGTGGCCATAAGACAGCCAACTACTATG 300
Db 377 TACCTGTAGGGTGTCTCACATATTCACTCCCTCATGTCAGTCGCTGTGAGT 556

Qy 301 CAGATCTTAAGATTCCTCCCAATGGGATCCACATTCTACCTGGAGATGACATTCT 360
Db 377 CAGATCTTAAGATTCCTCCCAATGGGATCCACATTCTACCTGGAGATGACATTCT 709

Qy 361 CAGATGTACTCTCGGAAGCAGGCCTATTCTGGAGACAAAGGCAAGAGGAAA 420
Db 377 CAGATGTGTCTGTGAATCAGACCTATTCTGGAGACAAAGGCAAGAGGAAA 769

Qy 421 ACCAA-GGGAAAGGAAAGAAAACCCACAGCTGAGAACCCCACCTGTGA 477
Db 377 ACCAAGGGAAAGGAAAGGGAGGTAGAAACTCACAGACTGAGAACCCCACCTGTGA 827

RESULT 10
LOCUS BI663772 744 bp mRNA linear EST 12-SEP-2001
DEFINITION 603288511F1 NCI_CGAP_Mam6 Mus musculus cDNA clone IMAGE:5322603 5'_mRNA sequence.
ORGANISM Mus musculus (house mouse)
ACCESSION BI663772
VERSION BI663772.1 GI:15578005
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
DEFINITION Mus musculus
MATERIALS Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Metazoa; Eukaryota; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
TISSUE Procurement: Gilbert Smith, Ph.D.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC Clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov

REFERENCE 1 (bases 1 to 744)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgabbs-r@mail.nih.gov
 Tissue Procurement: Jeffrey Green M.D.
 cDNA Library Preparation: Life Technologies, Inc.
 DNA Sequencing by: The I.M.A.G.E. Consortium
 Clone distribution: Incyte Genomics, Inc.
 Found through the I.M.A.G.E. Consortium/LINL at:
 http://image.lnl.gov
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FEATURES source

1. 744 Location/Qualifiers

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 /clone="IMAGE:5322603"
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 /clone="NCI-CGAP Mam6"

Note= "Organ: mammary; Vector: PCMV-SPORT6; Site: 1; Sali; Site 2: Not I; Cloned unidirectionally; Primer: Oligo dR. Library constructed by Life Technologies. Investigator providing samples: Jeffrey Green, M.D., NIH"

ORIGIN

Query Match	84.4%	Score 402.4;	DB 1.2;	Length 744;
Best Local Similarity	92.2%	Pred. No. 1.6e-100;		
Matches	435;	Conservative	0;	Mismatches 36;
		Indels	1;	Gaps 1;

Db 107 ATGGTGGCCATGAGCTTGTCACTTGTGCTTCAAGGTCTTAGTGCTTGCTGCACT 60
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 Qy 61 TCCCCGGGGCCCTGTCTCTGGAAACACTCACAGAATGGAAAGTGTGCCTTCAT 120
 Db 167 TCCCA-GEGCCCTGTCTGTCTGGAAACACTCACAGAATGGAAAGTGTGCCTTCAC 225
 Qy 121 GAATGTGGGGCCCAAGGTACTGCGGGCAATGGAGACTGTGATTCGGAGATAA 180
 Db 226 GAATGTGGGTGCGAGCTACTGTGGGCCATGGAGCTGTGATCTGGATGA 285
 Qy 181 CACCTTAATGAAAGTGTCTCATATATTGTCGGCTCATGTGCTTCCTCGAGTCGCTGTAGT 240
 Db 286 TACCTGTAGGGTGTACATATTGTCCTCGAGTCGCTGTAGT 345
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 Db 346 GGCTGCTTGGTGAAGTGGCTGGATGAAAGTGTGCTGCACTGGCCATAAAGCAGCACTCACTAGT 405
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 Db 406 CAGATCTTAAGTTCCCAATCGGATCCACATTCTACGGGAGATGACATTCT 465
 Qy 361 CAGGATGACTCTGGAATGAGGCTTATCTGGAGACGACAAGGCAAAAGGAA 420
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 Qy 421 ACCAAGGGAAAGGAAAGCAGCAAAGCAAAACCCCAAGACTGAGGAACCCACC 472
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 Qy 681 GGCTGCTTGGTGAAGGAGGGCTTGGCTGAGCTGGCGCCAAATGGAGAGCTGCTGATCGATTCAC 300
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 Qy 801 CAGATCTTAAGATTCCCCAAATGGGATCCACATTCTGGAGATGACATTCT 360

RESULT 11
 AI272466 LOCUS AI272466
 DEFINITION ukOC06.y1 Schiller mouse MAC13 mRNA linear EST 18-NOV-1998
 mRNA similar to gb:X80171 M.musculus P1GF mRNA
 (MOUSE); mRNA sequence.
 AI272466 GR:3894734
 ACCESSION AI272466.1
 VERSION

was made by oligo-dT priming and size-selected by column fractionation. Libraries were amplified once on solid support and plasmid DNA from each library was prepared and mixed in equal amounts. The mixed library DNA was normalized by method #4 from Bonaldo, Lennon, and Soares (1996) Genome Research 6:791-806. 0.5 microgram

GINN AND COMPANY, BOSTON, MASS.

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Query Match      75.7%; Score 361.2; DB 12; Length 489;
Best Local Similarity 92.0%; Pred. No. 3.6e-89;
Matches 381; Conservative 0; Mismatches 33; Indels 0; Gaps 0
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123

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244	TGCTGTGGTGAAGGAGTTCTGCACTGTGGCCTAAGACGCCAACTACATATGAG 3.03
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SULT 1A
 583990 CFS82990 958 bp mRNA linear EST 24-SEP-2003
CUTS AGENCOUNT 111363121 - updated NIH_MGC_137 Mus musculus cDNA clone
DEFINITION IMAGE:6132281 5 , mRNA sequence.
IMAGE:6132281

CF582990
 CF582990.1
 EST.
 WORDS
 SOURCE
 ORGANISM
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mus musculus (house mouse)
 Mammalia; Eutheria; Rodentia; Muridae; Murinae; Mus;
 1 (basses 1 to 958)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999).
VOLUME
PAGENUMBER
COMMENT
CONTACT: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm1007 Bethesda, MD 20892
Email: crabbs@mail.nih.gov

Tissue: Human Endocrine Pancreas
Tissue Procurement: Gerard Gradwohl (PNAS 97 P1607-1611, 2000)
CDNA Library Preparation: Catherine Lee, Endocrine Pancreas Consortium
CDNA Library Arrayed by: The I.M.A.G.B. Consortium (LlNL)
DNA sequencing by: Agencourt Bioscience Corporation
Clone distribution: MacClelland distribution information can be found at www.genome.wustl.edu

found through the IMAGE Consortium/LINI at:

Downloaded through the U.S. Consular Library at:
<http://image.llnl.gov>
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High quality sequence stop: 537.
Location/Qualifiers

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  /clone_lib="NIH MGC 137"
  /note="Organ: Pancreas Vector: pSPORT1; Site:1; Sali;
Site:2; NotI; Library consists of a pool of clones
rearranged from the following libraries: Melton normalized
mixed mouse pancreas 1, NI-MMS1, Amplified Melton mouse
islets 1, M1S1-A, and Kaestner ngn3 wt. Clones rearranged in
the laboratory of F.K. Kaestner (University of
Pennsylvania). Note: this is a NIH MGC Library."

```

Tissue Procurement: Lothar Hennighausen Ph.D., Chu-Xia Deng Ph.D.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNNL)
CNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNNL at:
<http://image.lnnl.gov>
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 High quality sequence stop: 788.
Location/Qualifiers
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/Site 2: Not I; Cloned: unidirectional; Primer: Oligo dr.
/Library constructed by Life Technologies. Investigators providing samples: Lothar Hennighausen, Chu-Xia Deng, NIH Reference for transgenic model: Xu et al., Nature Genetic 22: 37-43 (1999)."

DEBTGIN

Query	Match	Score	Length
Best Local Matches	ATGTCGGCCATGAACCTGTCACTTGCTTCTAGCGGTCTAGCTGGTGGC	75.2%	908
Local Similarity	Pred. No. 2.1e-88;	90.0%	
Conservative	0; Mismatches -42;		Indels 6;
Matches 430;			
2y	1 ATGTCGGCCATGAACCTGTCACTTGCTTCTAGCGGTCTAGCTGGTGGC		
Db	314 ATGTCGGTCACTGGCTCTGGCTGCTGCTGCTTCAAGCTGGTGGC		
2y	61 TCCAGGGGCCCTCTGCTGGACAACTCAAAGAAATGAAATGGCC		
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2y	121 GAACTGGGGCCGGAGCTACTGGGGCAATGGAGAAAGCTGGTGPACATGCG		
Db	434 GAACTGGGGCTGGCTGAGCTACTGTCGGCCATGGAGAGCTGGTGPACATCTT		
Qy	181 CACCCTAATGAACTGTCATATACTGCGTCAATGTCATGTCCTCTGAGTCG		
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Qy	241 GGCTGTGTGTGTGAGGGGTGCGACTGTGCGCTAAAGACGCCAACAT		
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Qy	301 CAGATCTTAAG-ATTCCCCCAATCGGATTCACATTCTGAGATGAA		
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Qy	417 GAAACCAAGGGAAA-GGAAGCAAAACCCACACACTGAGGAACCC		

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Job time : 2002 secs

(OLIGO) 72245 24/2/67

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 16, 2004, 19:52:00 ; Search time 64 Seconds

4136.118 Million cell updates/sec
4136.118 Million cell updates/sec

Title: US-10-071-370A-3

Perfect score: 477

Sequence: 1 atgctggccatgaactgttt.....ctgaggaaacccaccgtgtga 477

Scoring table: IDENTITY_NUC

Gapext 1.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365419

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	477	100.0	477	3	US-08-586-039B-38
2	477	100.0	477	4	US-09-699-769-38
3	414	86.8	417	3	US-08-586-039B-36
4	414	86.8	417	4	US-09-699-769-36
5	230.2	48.3	513	3	US-08-586-039B-44
6	230.2	48.3	513	4	US-09-699-769-44
7	229.8	48.2	465	4	US-08-596-039B-40
8	229.8	48.2	465	4	US-09-699-769-40
9	213.6	44.8	1645	2	US-08-039-297B-1
10	213.2	44.7	450	3	US-08-586-039B-46
11	213.2	44.7	450	4	US-09-699-769-46
12	108.8	22.8	677	3	US-08-718-904-3
13	108.8	22.8	677	4	US-09-449-249-3
14	108.8	22.8	677	5	PCT-US5-1093A-27
15	108.8	22.8	728	3	US-08-718-904-4
16	108.8	22.8	728	4	US-09-449-249-4
17	108.8	22.8	728	5	PCT-US5-1093A-28
18	107.2	22.5	495	4	US-09-037-983C-14
19	107.2	22.5	516	3	US-08-784-551C-1
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21	107.2	22.5	516	4	US-09-708A-3
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23	107.2	22.5	516	4	US-09-428-909A-1
24	107.2	22.5	516	4	US-09-392-931-3
25	107.2	22.5	545	4	US-09-244-583-1
26	107.2	22.5	642	4	US-09-192-932-9
27	107.2	22.5	642	4	US-09-374-708A-7

RESULT 1
US-08-586-039B-38
; Sequence 38, Application US/08586039B
; Patent No. 6140073
; GENERAL INFORMATION:
; APPLICANT: Bayne, Marvin L.
; ADDRESS: Thomas Jr., Kenneth A.
; TITLE OF INVENTION: VASCULAR ENDOTHELIAL CELL GROWTH FACTOR C
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merck & Co., Inc.
; STREET: 126 E. Lincoln Avenue
; CITY: Rahway
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07065-0900
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Microsoft Word 6

CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/586-039B
; FILING DATE: 16-JAN-1996
; CLASSIFICATION:
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 08/124,259
; FILING DATE: 20-SEP-1993
; APPLICATION NUMBER: 07/676,436
; FILING DATE: 28-MAR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Hand, J. Mark
; REGISTRATION NUMBER: 36,545
; REFERENCE/DOCKET NUMBER: 18361DA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 594-3905
; TELEFAX: (908) 594-4720
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 477 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-586-039B-38

Query Match Score 477; DB 3; Length 477;
Best Local Similarity 100.0%; Pred. No. 9.8e-149;
Matches 477; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CLASSIFICATION:
 PRIORITY APPLICATION DATA: 08/124,259
 FILING DATE: 20-SEP-1993
 APPLICATION NUMBER: 07/676,436
 FILING DATE: 28-MAR-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Hand, J. Mark
 REGISTRATION NUMBER: 36,545
 REFERENCE/DOCKET NUMBER: 1B361DA
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (908) 594-3905
 TELEFAX: (908) 594-4720
 STRANDBNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 US-08-699-039B-36

Query Match 86.8%; Score 414; DB 3; Length 417;
 Best Local Similarity 100.0%; Pred. No. 8.1e-128;
 Matches 414; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGCTGGCATGAACTGTTACTGTGTTACTGTGTTAGCTGGTGTGAC 60
 Db 1 TCCCAAGGGGCCCTGTCGTGGAAACAATCAACAGAAATTGAAAGTGGCCCTTCAT 120
 Qy 61 TCCCAAGGGGCCCTGTCGTGGAAACAATCAACAGAAATTGAAAGTGGCCCTTCAT 120
 Db 61 TCCCAAGGGGCCCTGTCGTGGAAACAATCAACAGAAATTGAAAGTGGCCCTTCAT 120

Qy 121 GAAGTGTGGGCCGAGCTACTGGCGGCCATGGCTGTTACATGGCAGATGA 180
 Db 121 GAAGTGTGGGCCGAGCTACTGGCGGCCATGGCTGTTACATGGCAGATGA 180

Qy 181 CACCTTAATGAACTGCTCATATAATTCACTGTCGTTATGTCGTTCTGACTCGCTGTAGT 240
 Db 181 CACCTTAATGAACTGCTCATATAATTCACTGTCGTTATGTCGTTCTGACTCGCTGTAGT 240

Qy 241 GGCTGTGTGTGTGACTGTGGCTCATATTCAGTCGTTATGTCGTTCTGACTCGCTGTAGT 300
 Db 241 GGCTGTGTGTGTGACTGTGGCTCATATTCAGTCGTTATGTCGTTCTGACTCGCTGTAGT 300

Qy 301 CAGATCTAAAGATTCCCCCAATCGGATCCACATTCCTACCTGGAGATGACATTCT 360
 Db 301 CAGATCTAAAGATTCCCCCAATCGGATCCACATTCCTACCTGGAGATGACATTCT 360

Qy 361 CAGGTGTCTCTGCAATGAGGCCTATCTGGAGAGCAGAACGGAAAGG 414
 Db 361 CAGGTGTCTCTGCAATGAGGCCTATCTGGAGAGCAGAACGGAAAGG 414

RESULT 4
 US-08-699-769-36
 Sequence 36. Application US/09699769
 ADDRESSEE: Merck & Co., Inc.
 Parent No. 6569434
 GENERAL INFORMATION:
 APPLICANT: Bayne, Marvin L.
 Thomas Jr., Kenneth A.
 TITLE OF INVENTION: VASCULAR ENDOTHELIAL CELL GROWTH FACTOR
 NUMBER OF SEQUENCES: 49
 C SUBUNIT C SUBUNIT

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Microsoft Word 6
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/699,769
 FILING DATE: 30-Oct-2000
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/1586,039
 FILING DATE: 16-JAN-1996
 APPLICATION NUMBER: 08/124,259
 FILING DATE: 20-SEP-1993
 APPLICATION NUMBER: 07/676,436
 FILING DATE: 28-MAR-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Hand, J. Mark
 REGISTRATION NUMBER: 36,545
 REFERENCE/DOCKET NUMBER: 1B361DA
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (732) 594-3905
 TELEFAX: (732) 594-4720
 INFORMATION FOR SEQ ID NO: 36:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 417 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 SEQUENCE DESCRIPTION: SEQ ID NO: 36:
 US-09-699-769-36

Query Match 86.8%; Score 414; DB 4; Length 417;
 Best Local Similarity 100.0%; Pred. No. 8.1e-128; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGCTGGCCATGAACTGTTACTGTGTTACTGTGTTAGCTGGTGTGAC 60
 Db 1 ATGCTGGCCATGAACTGTTACTGTGTTACTGTGTTAGCTGGTGTGAC 60

Qy 61 TCCCAAGGGGCCCTGTCGTGGAAACAATCAACAGAAATTGAAAGTGGCCCTTCAT 120
 Db 61 TCCCAAGGGGCCCTGTCGTGGAAACAATCAACAGAAATTGAAAGTGGCCCTTCAT 120

Qy 121 GAAGTGTGGGCCGAGCTACTGGCGGCCATGGCTGTTACATGGCAGATGA 180
 Db 121 GAAGTGTGGGCCGAGCTACTGGCGGCCATGGCTGTTACATGGCAGATGA 180

Qy 181 CACCTTAATGAACTGCTCATATAATTCACTGTCGTTATGTCGTTCTGACTCGCTGTAGT 240
 Db 181 CACCTTAATGAACTGCTCATATAATTCACTGTCGTTATGTCGTTCTGACTCGCTGTAGT 240

Qy 241 GGCTGTGTGTGTGACTGTGGCTCATATTCAGTCGTTATGTCGTTCTGACTCGCTGTAGT 300
 Db 241 GGCTGTGTGTGTGACTGTGGCTCATATTCAGTCGTTATGTCGTTCTGACTCGCTGTAGT 300

Qy 301 CAGATCTAAAGATTCCCCCAATCGGATCCACATTCCTACCTGGAGATGACATTCT 360
 Db 301 CAGATCTAAAGATTCCCCCAATCGGATCCACATTCCTACCTGGAGATGACATTCT 360

Qy 361 CAGGTGTCTCTGCAATGAGGCCTATCTGGAGAGCAGAACGGAAAGG 414
 Db 361 CAGGTGTCTCTGCAATGAGGCCTATCTGGAGAGCAGAACGGAAAGG 414

RESULT 5
 US-08-586-039B-44
 Sequence 44. Application US/08586039B
 ADDRESSEE: Bayne, Marvin L.
 Street: 1226 E. Lincoln Avenue
 City: Rahway
 State: New Jersey
 Country: USA
 ZIP: 07065-0900
 COMPUTER READABLE FORM:

GENERAL INFORMATION:
 APPLICANT: Bayne, Marvin L.
 Thomas Jr., Kenneth A.
 TITLE OF INVENTION: VASCULAR ENDOTHELIAL CELL GROWTH FACTOR C

TITLE OF INVENTION: SUBUNIT
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merck & Co., Inc.
STREET: 126 E. Lincoln Avenue
CITY: Rahway
STATE: New Jersey
COUNTRY: USA
ZIP: 07065-0900

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Microsoft Word 6
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/586,039B
FILING DATE: 16-JAN-1996
CLASSIFICATION:
PRIORITY APPLICATION NUMBER: 08/124,259
FILING DATE: 20-SEP-1993
APPLICATION NUMBER: 07/676,436
FILING DATE: 28-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Hand, J. Mark
REGISTRATION NUMBER: 36,545
REFERENCE/DOCKET NUMBER: 18361DA
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-3905
TELEFAX: (908) 594-4720
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 513 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-586-039B-44

Query Match 48.3%; Score 230.2; DB 3; Length 513;
Best Local Similarity 71.6%; Pred. No. 1.2e-66;
Matches 336; Conservative 0; Mismatches 118; Indels 15; Gaps 2;

Db 1 ATGCTGCCATGAGCTGTACTTGCATGGCTCTAGTGCTGGCTGTGCAC 60
1 ATGGGGTATGAGGTGTTCCCTGTTCTGAGCTCTGCGCCGGCTGGCTGGCT 60

Qy 61 TCC-----CAGGGGGCCCTGCTGCTGGAAACAACCAACGAATAAAGGAACTG 108
Db 61 GCTGTGCCCCCCAGAAGGGCTTGTGCTGGAAAGGGCTGTCAGGGTAATG 120

Qy 109 GTGCTTTCATGAGTGGGGCCGCACTACTGGAAAGCTGGTGTAC 168
Db 121 GTACCTTCAGGAAACCCPATGAAGTGTCTCATATATTCAGTCGGTATGTGCTTCCTG 228

Qy 169 ATTCAGATGAAACCCATGAGCTGGGCTGGAAAGGGCTGGAACTG 288
Db 181 GTGCTGTCGAGTGGCTGGAAAGGGCTGGAACTGAGCTGGAACTGGTCTCCCTG 240

Qy 229 AGTCGCTTAGTGGCTGGCTGTGGCTGGAGGCTTAAGAACAGCC 357
Db 241 CTGGCTGACCGCTGGCGGATAGAAATCTGCCTGCGGCTGTGGCTGGAAAGGCC 300

Qy 289 AACATCACATGAGATCTTAAAGATGCCCAATGGGATCCACATTCCTACGTGAG 348
Db 301 AATCTCACATGAGCTTAAAGATGCCCAATGGGATCCACATTCCTACGTGAG 357

Qy 349 ATGACATCTCTGGATGTTACTCTGCCTGGCTGGCTGGCTGGAAAGGCC 408
Db 358 CTGAGCTTCTCTGCACTTCTGCAATGCGGCTCTGGCTGGAAAGTGAAASC 417

Qy 409 GAAAGGAGAAAACCAGGGAGAAGGAAAGAACCCACAGA 457
Db 418 GAAAGGAGGAGACCCAAAGGGCAGGGGGAAAGGGAGAGAGAGCAGA 466

RESULT 6
US-09-699-769-44
Sequence 44, Application US/09699769
Patent No. 6569314
GENERAL INFORMATION:
APPLICANT: Bayne, Marvin L.
Thomas Jr., Kenneth A.
TITLE OF INVENTION: VASCULAR ENDOTHELIAL CELL GROWTH FACTOR
C SUBUNIT
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merck & Co., Inc.
STREET: 126 E. Lincoln Avenue
CITY: Rahway
STATE: New Jersey
COUNTRY: USA
ZIP: 07065-0900
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Microsoft Word 6
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/693,769
FILING DATE: 30-Oct-2000
CLASSIFICATION: <Unknown>
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/586,039
FILING DATE: 16-JAN-1996
APPLICATION NUMBER: 08/124,259
FILING DATE: 28-MAR-1993
APPLICATION NUMBER: 07/676,436
FILING DATE: 28-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Hand, J. Mark
REGISTRATION NUMBER: 36,545
REFERENCE/DOCKET NUMBER: 18361DA
TELECOMMUNICATION INFORMATION:
TELEPHONE: (732) 594-3705
TELEFAX: (732) 594-4720
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 513 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 44:
US-09-699-769-44

Query Match 48.3%; Score 230.2; DB 4; Length 513;
Best Local Similarity 71.6%; Pred. No. 1.2e-66;
Matches 336; Conservative 0; Mismatches 118; Indels 15; Gaps 2;

Db 1 ATGCTGCCATGAGCTTCATGGCTCTAGTGCTGGCTGTGCAC 60
1 ATGGGGTATGAGGTGTTCCCTGTTCTGAGCTCTGCGCCGGCTGGCTGGCT 60

Qy 61 TCC-----CAGGGGGCCCTGCTGCTGGAAACAACCAACGAATAAAGGAACTG 108
Db 61 GCTGTGCCCCCCAGAAGGGCTTGTGCTGGAAAGGGCTGTCAGGGTAATG 120

Qy 109 GTGCTTTCATGAGTGGGGCCGCACTACTGGAAAGCTGGTGTAC 168
Db 121 GTACCTTCAGGAAACCCPATGAAGTGTCTCATATATTCAGTCGGTATGTGCTTCCTG 228

Qy 169 ATTCAGATGAAACCCATGAGCTGGGCTGGAAAGGGCTGGAACTG 288
Db 181 GTGCTGTCGAGTGGCTGGCTGTGGCTGGAGGCTTAAGAACAGCC 300

Qy 229 AGTCGCTTAGTGGCTGGCTGTGGCTGGAGGCTTAAGAACAGCC 357
Db 241 CTGGCTGACCGCTGGCGGATAGAAATCTGCCTGCGGCTGTGGCTGGAAAGGCC 300

Qy 289 AACATCACATGAGATCTTAAAGATGCCCAATGGGATCCACATTCCTACGTGAG 348
Db 301 AATCTCACATGAGCTTAAAGATGCCCAATGGGATCCACATTCCTACGTGAG 357

Qy 349 ATGACATCTCTGGATGTTACTCTGCCTGGCTGGCTGGAAAGGCC 408
Db 358 CTGAGCTTCTCTGCACTTCTGCAATGCGGCTCTGGCTGGAAAGTGAAASC 417

Qy 409 GAAAGGAGAAAACCAGGGAGAAGGAAAGAACCCACAGA 457
Db 418 GAAAGGAGGAGACCCAAAGGGCAGGGGGAAAGGGAGAGAGAGCAGA 466

RESULT 7
US-08-586-039B-40
; Sequence 40, Application US/08586039B
; Patent No. 6140073
; GENERAL INFORMATION:
; ADDRESSEE: Merck & Co., Inc.
; STREET: 126 E. Lincoln Avenue
; CITY: Rahway
; COUNTRY: USA
; ZIP: 07065-0900
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Microsoft Word 6
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/586,039B
; FILING DATE: 16-JAN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hand, J. Mark
; REGISTRATION NUMBER: 36,545
; REFERENCE/DOCKET NUMBER: 18361DA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 594-3905
; FAX: (908) 594-4720
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 465 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-586-039B-40

Qy 229 AGTCGCTGTAGTGGCTGCTGTGTGACGAGGGCTCTGGCACTGCTGGCTAAAGACAGCC 288
Db 241 CTGCGCWSACCCGCGCTGTGGCGATGAAATCGACTGTTGCGGTGAGACGCC 300
Qy 289 AACATCACTATGGAGATCTTAAGATTCCCAATCGGANTCACATTCTAACGTGAG 348
Db 301 AATGTCACCATGAGGCTCTAAGAT--CCGTTCTGGGACCGGCTCTCTACGTGGAG 357
Qy 349 ATGACATCTCTAGGATGACTCTGGCAATGGGGCTTATCTGGAGAACGACAAGCC 408
Db 358 CTGACGTTCTCTAGCACTGGCTCTGGGCAATGCGGCCATGGTGAAGATGAAGCCG 417
Qy 409 GAAGGAGAAACCAAGGGAAAGGGAAAGGAAACACCCACACA 457
Db 418 GAAAGGAGAAAGCCAAGGGCAAGGGAAAGGAGAGGAGAGGAGAGGAGA 466

RESULT 8
US-09-639-769-40
; Sequence 40, Application US/096399769
; Patent No. 6569434
; GENERAL INFORMATION:
; APPLICANT: Bayne, Marvin L.
; TITLE OF INVENTION: VASCULAR ENDOTHELIAL CELL GROWTH FACTOR C
; NUMBER OF SEQUENCES: 49
; TITLE OF INVENTION: SUBUNIT
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merck & Co., Inc.
; STREET: 126 E. Lincoln Avenue
; CITY: Rahway
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07065-0900
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Microsoft Word 6
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/639,769
; FILING DATE: 20-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Hand, J. Mark
; REGISTRATION NUMBER: 36,545
; REFERENCE/DOCKET NUMBER: 18361DA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 594-3905
; FAX: (908) 594-4720
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 465 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-586-039B-40

Qy Match Score 229.8; DB 3; Length 465;
Best Local Similarity 72.3%; Pred. No. 1.5e-66;
Matches 332; Conservative 0; Mismatches 112; Indels 15; Gaps 2;

Qy 1 ATGCTGGCCATGAAAGCTGTGACTCTGGCTTGTGCACTGCTAGCTGGTGTGCACTGAC 60
Db 1 ATGCGCTCATGAGGCTGTCCCTGTTCTGAGCTCTGGCGGGTGGCGCTGGCT 60
Qy 61 TCC-----CAGGGGCCCCCTGTCGTGGAAACACTCAACAGAAAATGGAAAGTG 108

61 GCTGTGCCCCCCCAGGAGTGGCTTGTGGAAAGGGCTCTGCTGGAAAGTG 120
62 Db Qy 109 GTCCTTCATAAAGTGTGGCCATGCTGGCTGCAATGGAAAGCTGTGAC 168
63 Db Qy 121 GTCACCTCCAGAAGTGGGGCTGGGCGCTGAGCTGCGCTGGCTGGAC 180
64 Db Qy 169 ATTCGAGATGAAACCCCTAATGAAAGTGTCTATATATCAAGTGCCTATGTGTCCTCTG 228
65 Db Qy 181 GTCGTGTCGAGTAACTGGCTGAGCTGGCTGAGGAGCATGTCAGCCATCTGTGTCCTCTG 240
66 Db Qy 229 ATGGCTGTAGTGGCTGCTGCTGACTGTGGCTTAAGACGCC 288
67 Db Qy 241 CTGGCTGACCGGCTGTGCGGCGATGAGAATCTGACTGTGCGGCTGAGACGCC 300
68 Qy 289 AACATCACTATGGAGATCTTAAGATCTGGAGAACGACAAGCC 348
69 Db Qy 301 AATGTCACCATGAGCTCTAAAGAT--CGTGTGGACGGCTCTAGTGGAG 357
70 Db Qy 349 ATGACATCTCTAGGATGACTCTGGCAATGGGGCTTATCTGGAGAACGACAAGCC 408
71 Db Qy 358 CTGACGTTCTCTAGCACTGGCTCTGGGCAATGCGGCCATGGTGAATGGGAGAGATGAAGCCG 417
72 Qy 409 GAAGGAGAAACCAAGGGAAAGGGAAAGGAAACACCCACACA 447
73 Db Qy 418 GAAAGGAGAAAGCCAAGGGCAAGGGAAAGGAGAGGAGAGGAGA 456

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TOPOLOGY: Linear
 MOLECULE TYPE: DNA (genomic)
 SEQUENCE DESCRIPTION: SEQ ID NO: 40:
 US-09-699-769-40

Query Match	Score 48.2%	Length 465;
Best Local Similarity 72.3%;	Pred. No. 1.5e-65;	
Matches 332;	Mismatches 112;	Indels 15;
Conservative 0;	Gaps 2;	
Qy 1 ATGCTGCCATGAAGGTGTTACTGGTTCCTAGCTGGTGCAC 60		
Db 1 ATGCCGTCATGAGGTGTTCCCTTGAGCTCCGGCGCTGGGCT 60		
Qy 61 TCC-----CAGGGGCCCTGTCCTGGAAACAATCACAGAAATGGAGTG 108		
Db 61 GCTGTCCCCCCAGGAGTGGCTGTCCTGGAAACGGCTGTAGCTGGAGTG 120		
Qy 109 GTGCCATTCAATGAAGTGTGGGCCAGCTGGCGCAATGGAGAACCTGGTAC 168		
Db 121 GTACCTTCAGGAACTGTGGGCCAGCTACTGGCGCTGGTGGAC 180		
Qy 169 ATTGGATGAACCTTAATGAAGTGTCTATATAATTCACTGGTCACTGTGTCCTG 228		
Db 181 GTGCCATTCAATGAAGTGTGGGCCAGGGAGAACATTTCAACCCATTCTGTGTCCTG 240		
Qy 229 AGTCTGGTACTGGCTGTGGTGAGGGCTCACTGTGTGGCTAAAGAGAGCC 288		
Db 241 CTGCGGTGACGGGCTGGGGATGAGATCTCACTGTGGGGTGGAGGGCC 300		
Qy 289 AACATACATGGCACATCTTAAGATTCGGGATCCAGGGATCCAGATCTTAGGGAG 348		
Db 301 AATGTCACCATGCACTTCCTAAAGAT--CCGTTCTGGAAACGGGCTCTAGGGAG 357		
Qy 349 ATGAAATTCTCAAGATGFACTCTCGAATGCAACGCCATTCTGGAGCGACAAAGCCA 408		
Db 358 CTGACTTTCTCAAGCTGGATGAGCTGGAGCTGGAGCTGGAGAGATGAGCCG 417		
Qy 409 GAAAGGAGAAAAACCAGGGAAAGAGGAACAAAGAAA 447		
Db 418 GAAAGGAGACCAAGGGAGGGAAAGGGAGAGA 456		

RESULT 9
 US-08-039-297-B-1
 Sequence 1; Application US/08039297B
 ; Patent No. 5919819
 GENERAL INFORMATION:
 ; APPLICANT: PERSICO, MARIA
 ; APPLICANT: MAGLIONE, DOMENICO
 ; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES CODING FOR A
 ; TITLE OF INVENTION: HUMAN
 ; TITLE OF INVENTION: PROTEIN WITH ANGIOGENESIS REGULATIVE PROPERTIES
 ; NUMBER OF SEQUENCES: 8
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: BEVERIDGE, DEGRANDI, WETLACHER & YOUNG,
 ; ADDRESSEE: L.L.P.
 ; STREET: 1850 M Street, N.W.
 ; CITY: Washington
 ; STATE: DC
 ; COUNTRY: USA
 ; ZIP: 20036
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/039,297B
 FILING DATE: 19-APR-1993
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 1.48315-A90
 FILING DATE: 27-SEP-1990

/ ATTORNEY/AGENT INFORMATION:
 / NAME: Weilacher, Robert G
 / REGISTRATION NUMBER: 20,531
 / REFERENCE/DOCKET NUMBER: 48573
 / TELECOMMUNICATION INFORMATION:
 / TELEPHONE: 202-659-2811
 / TELEFAX: 202-659-1462
 / TELEX: WU164470
 / SEQUENCE CHARACTERISTICS:
 LENGTH: 1645 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-08-039-297B-1

	Query	Match	Score	Length	DB	2;	Score	Length	DB	2;	Score	Length	DB	2;
	Qy	1	ATGTTGGCATGAGCTGGTCACTGGCTTGGGCTAGCTGGGTGGCTGGCTGGCAC	60			213.6	1645;	1		7.5e-61		15;	Gaps
	Db	322	ATGCGGTATGAGCTGGTCCCTTGCTTCTGAGCTGGCTGGCTGGCTGGCT	381			0;	Mismatches	139;	Indels	15;		2;	
	Qy	61	TCC-----CAGGGGGCCCTGTCGTCGCTGGACAAACTCAACAGAAATGGAACTG	108										
	Db	382	GCTGTGCCGCCAGAAGGGCTTGCTGCCTGAGCGGCTGAGGGAACTGGAAGCTG	441										
	Qy	109	GTCGCTTCATGAACTGTCGGGGCCGAGCTACTGGGCCAATGGACAGCTGGTAC	168										
	Db	442	GTACCCCTCCAGGAGCTGGGGCCGGAGCTACTGGCGGCTGGAGGGCTGGAC	501										
	Qy	169	ATTCGAGATGAAACCCPAATGAAAGTGGCTCATATACTTCACTGGCTTCTG	228										
	Db	502	GTCTGTCTGGTAGTACCCAGGGCTGGAGGCACTGGCTGGCTGGAGGCA	561										
	Qy	229	AGTCGCTGTAGTGGCTGGTGAAGGAGGTCTGCACTGTGGCTTAAGAACAGCC	288										
	Db	562	CTCGGCTGACCGCTGTCGECGATGAGAACTGCACTGTGGCTGGAGAACGCC	621										
	Qy	289	AACATCACTATGGAGACTTAAAGATTCCTCCCAAATGGATCCACATTCTACAGTGAG	348										
	Db	622	AATGTCACCATGAGCTCTAAAGAT---CCGGTTCTGGGACGGGCTCTACAGTGAG	678										
	Qy	349	ATGACATCTCTGAGGTACTCTGGCAATGGGGCTATTCTGGAGACAAGGCCA	408										
	Db	679	CTGAGCTCTCTGAGCTGGCAATGGGGCTCTGGAGAATGAGAGTCAGCGCG	738										
	Qy	409	GAAAGGAGGAAACCAAGGGAAAGGAAAGGAAAACCCCAAGACTGGAAACCC	468										
	Db	739	GAAAGGTCGGGAGATGCTTCCCGAGGTAACCCACCCCTGGAGGAGAACCCG	798										
	Qy	469	CACCTG 474											
	Db	799	CACCCG 804											

RESULT 10
 US-08-586-039B-46
 / Sequence No. 46, Application US/08586039B
 / Patent No. 6140073
 / GENERAL INFORMATION:
 / APPLICANT: Barrie, Marvin L.
 / INVENTOR: Thomas Jr., Kenneth A.
 / TITLE OF INVENTION: VASCULAR ENDOTHELIAL CELL GROWTH FACTOR C
 / NUMBER OF SEQUENCES: 49
 / CORRESPONDENCE ADDRESS:
 / ADDRESSEE: Merck & Co., Inc.
 / STREET: 126 E. Lincoln Avenue
 / CITY: Rahway
 / COUNTRY: USA

ZIP: 07065-0900
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Microsoft Word 6
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/586, 039B
 FILING DATE: 16-JAN-1996
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Hand, J. Mark
 REGISTRATION NUMBER: 36,545
 REFERENCE/DOCKET NUMBER: 18361DA
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (908) 594-3905
 TELEFAX: (908) 594-4720
 INFORMATION FOR SEQ ID NO: 46:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 450 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 STRANGLITY: linear
 MOLECULE TYPE: DNA (genomic)
 S-08-586-039B-46

	Query Match	Score 213.2;	DB 3;	Length 450;
Y	Best Local Similarity 72.4%;	Pred. No. 5e-61;	Mismatches 0;	Gaps 2;
b	Matches 310; Conservative	Indels 15;		
b				
Y	1 ATGCTGCCATGAGCCTTCACTGGCTTCTGGAGGTTCTAGCTGGCTTGCGCTGTGCAC 60			
b	1 ATGCCGTCATGGCTTCCCTGGCTTCCTGGCTCTGGAGCTCTGGCGCTGGCTGCCT 60			
Y	61 TCC-----CAGGGGCCAGAATGGGGCTTGTGGCTTGTCTGGAAACACTAACAGAAATGAATG 108			
b	61 GCTGTGCCCCAGAATGGGGCTTGTGGCTTGTCTGGAAACAGCTCTCAAGGTGAAATG 120			
Y	109 GTGCCCTTCATGAAAGCTGGGGCCGGAGCTAATGCCGCGCAATGGAGAAGCTGGTAC 168			
b	121 GTACCTCTCCAGAAAGCTGGGGCCGGAGCTAATGCCGCGCAATGGAGAAGCTGGGAC 180			
Y	169 ATGGCAATGAAACCTTAATGAGTGTCTCATATACTAGTCCCTCATATGTCCTCTG 228			
b	181 GTCGTGCGAGTAACCCAGCAGGTTGGAGCACATGTTGCGCCATCCCTGTCCTCTG 240			
Y	229 AGTCGCTTAGTGGCTAGTGGCTGGTGAAGGGGTCTGACTGTGTTGGCTAAAGAGAGCC 288			
b	241 CTGCGCTAACCGCTGCTGGGGATGAGAAATGCACTGTGGCTGGAGGGCC 300			
Y	289 AACATCCTATGCGATCTTAAAGATTCCCCAAATGGGATCCACATTCTACGGGAG 348			
b	301 AATGTCACCATGCGCTTAAAGAT--CCGTTCTGGGACCGGGCTCTACGGGGAG 357			
Y	349 ATGACATTCCTAGGATGTACTCTGGTGAATGCAAGGCTATTCTGAGACACAGGGCA 408			
b	358 CTGAGCTTCCTCAAGCACGTTGGTGAATGCCCTCTGCGGGAGAATGAGGCCG 417			
Y	409 GAAAGGGAG 416			
b	418 GAAGGTG 425			

RESULT 11
US-09-699-769-46
Sequence 46, Application US/09699769
GENERAL INFORMATION:

Qy 349 ATGACATCTCTCAGATGTACTCTCGAAATGAGCCATTCTGGAAAGGACAAGGCCA 408
 Db 358 CTGAAGTCTCACGTCGTCGATGCCCTCTGGAGAGATGAGCCCG 417

Qy 409 GAAAGGAG 416
 Db 418 GAAAGGTG 425

RESULT 12
 US-08-718-904--3
 Sequence 3, Application US/08718904
 / GENERAL INFORMATION:
 / NUMBER OF SEQUENCES: 128
 / APPLICANT: Baird, J. Andrew
 / ADDRESSEE: SED and BERRY LLP
 / CITY: Seattle
 / STATE: Washington
 / ZIP: 98104-7092
 / COMPUTER READABLE FORM:
 / MEDIUM TYPE: Floppy disk
 / COMPUTER: IBM PC compatible
 / OPERATING SYSTEM: PC-DOS/MS-DOS
 / SOFTWARE: PatentIn Release #1.0, Version #1.25
 / CURRENT APPLICATION DATA:
 / APPLICATION NUMBER: US/08/718,904
 / FILING DATE: 24-SEP-1996
 / CLASSIFICATION: 424
 / ATTORNEY/AGENT INFORMATION:
 / NAME: NO. 603739enburg Ph.D., Carol
 / REGISTRATION NUMBER: 39,317
 / REFERENCE/DOCKET NUMBER: 760100.415C1
 / TELECOMMUNICATION INFORMATION:
 / TELEPHONE: (206) 622-4900
 / TELEFAX: (206) 682-6031
 / INFORMATION FOR SEQ ID NO: 3:
 / SEQUENCE CHARACTERISTICS:
 / LENGTH: 677 base pairs
 / TYPE: nucleic acid
 / STRANDEDNESS: double
 / TOPOLOGY: both
 / MOLECULE TYPE: cDNA
 / FEATURE:
 / NAME/KEY: CDS
 / LOCATION: 13..657
 / OTHER INFORMATION: /product= "leader sequence-encoding DNA"
 / FEATURE:
 / NAME/KEY: CDS
 / LOCATION: 13..90
 / OTHER INFORMATION: /product= "leader sequence-encoding DNA"
 us-08-718-904-3

Query Match 22.8%; Score 108.8; DB 3; Length 677;
 Best Local Similarity 59.8%; Pred. No. 3..2e-26;
 Matches 201; Conservative 0; Mismatches 132; Indels 3; Gaps 1;

Qy 103 GAAGTGTTGCCCTTCATGAAAGTGTTGGGCCGAGCTACTGGCGCANATGAGAACCTG 162
 Db 127 GAAATGGAAAGTCATGATGCTATAGCCGAGCTATGCCATCATGAGCCCTG 186

Qy 163 GTGTACATGCGATGACACCCATAATTGAAATGTCATATTCATCGTCATGTC 222
 Db 187 GGAGACATCTTCAGGAGTACCTGATGAGCTACATTCAGCCATTCGTGTC 246

Qy 223 CTTCTGAGTCGCTGTAGTGGCTGCTGAGGAGTGTGACTGTGTCGCTAAAG 282

Db 247 CCCCTGATGGATGGGGCTGCTGCAATGACAGGGCTTAAGATTCACATCCACTGAG 306
 Qy 283 ACAGCCAACATCATCATGAGATCTTAAAGATTCACATCCACTGAGATCCACATCCTAC 342
 Db 307 GAGTCACATCACCATGAGATTCACATGCGATCAACCTCACCAGGCCAGCA -- CATA 363
 Qy 343 GTGGAGATGACATCTCGGGATGACTCTGCAGATGAGGCCTATTCGGAGAGACA 402
 Db 364 GGAGAGATGCTCTCATGACAAACAAATGTCATGAGACAAAGGATGAGAGCA 423

RESULT 13
 US-09-419-249-3
 / Sequence 3, Application US/09449249
 / Patent No. 6503886
 / GENERAL INFORMATION:
 / APPLICANT: Baird, J. Andrew
 / ADDRESSEE: SED and BERRY LLP
 / CITY: Seattle
 / STATE: Washington
 / ZIP: 98104-7092
 / COMPUTER READABLE FORM:
 / MEDIUM TYPE: Floppy disk
 / COMPUTER: IBM PC compatible
 / OPERATING SYSTEM: PC-DOS/MS-DOS
 / SOFTWARE: PatentIn Release #1.0, Version #1.25
 / CURRENT APPLICATION DATA:
 / APPLICATION NUMBER: US/09/449,249
 / FILING DATE: 24-No. 6503886-1999
 / CLASIFICATION: <Unknown>
 / PRIORITY APPLICATION DATA:
 / APPLICATION NUMBER: US/08/718,904
 / FILING DATE: 24-SEP-1996
 / ATTORNEY/AGENT INFORMATION:
 / NAME: NO. 6503886enburg Ph.D., Carol
 / REGISTRATION NUMBER: 39,317
 / REFERENCE/DOCKET NUMBER: 760100.415C1
 / TELECOMMUNICATION INFORMATION:
 / TELEPHONE: (206) 622-4900
 / TELEFAX: (206) 682-6031
 / INFORMATION FOR SEQ ID NO: 3:
 / SEQUENCE CHARACTERISTICS:
 / LENGTH: 677 base pairs
 / TYPE: nucleic acid
 / STRANDEDNESS: double
 / TOPOLOGY: both
 / MOLECULE TYPE: cDNA
 / FEATURE:
 / NAME/KEY: CDS
 / LOCATION: 13..657
 / OTHER INFORMATION: /product= "leader sequence-encoding DNA"
 / FEATURE:
 / NAME/KEY: CDS
 / LOCATION: 13..90
 / OTHER INFORMATION: /product= "leader sequence-encoding DNA"
 / SEQUENCE DESCRIPTION: SEQ ID NO: 3:
 US-09-419-249-3

Query Match 22.8%; Score 108.8; DB 4; Length 677;
 Best Local Similarity 59.8%; Pred. No. 3..2e-26;
 Matches 201; Conservative 0; Mismatches 132; Indels 3; Gaps 1;

RESULT 14
PCT-US95-10973A-27
Sequence 27, Application PC/TU9510973A
GENERAL INFORMATION:
APPLICANT: Prizm Pharmaceuticals, Inc.
TITLE OF INVENTION: CONJUGATES OF VASCULAR ENDOTHELIAL GROWTH FACTOR WITH TARGET
NUMBER OF SEQUENCES: 107
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/10973A
FILING DATE: 29-AUG-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Nottenburg, Carol
REGISTRATION NUMBER: 39,317
REFERENCE/DOCKET NUMBER: 760100.4139PC
TELEPHONE: (206) 682-4900
TELEFAX: (206) 682-6031
SEQUENCE CHARACTERISTICS:
LENGTH: 677 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: both
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 13..657
OTHER INFORMATION: /product= "VEGFI89-encoding DNA"
PCT-US95-10973A-27
Query Match

QY 103 GAATGGGTGCCTTCATGAAAGTGTGGGCCCGAGCTACTGGCGCAATGGAGAACGTG 162
Db 127 GAACTGGTGAATTCATGGATCTCATGAGTCGAGTACTGCATCAAATCGAACCTG 186
QY 163 GTCTACATTGGAGATGAAACCCCTTAATGAAAGTGTCTCATATAATTCACTCCGTCATGTC 222
Db 187 GTGACAACTCTCCAGGATACCTGTGATGAGTCGATCACCTCAAGCCATCCTGTGTG 246
Qy 223 CTCTCTGAGTCGCTGTGATGGCTGCTGTGGTGGAGGTCTGCACTGTTGGCTAAAG 282
Db 247 CCCCTGATGGATGCTGGGCTGCTGCAATGAGGGCTGAGTGTGGCCACCTGAG 306
Qy 283 ACAGCCAACTACATATGAGATCTTAAGATCCCCCATGGGATCCACATCTCTAC 342
Db 307 GAGTCGCAACATGAGATCTGGGATCAAACCTCAAAAGGCA---CTATA 363
Qy 343 GTGGAGATGCAATTCTCGGGATGTTACTCTGGGAATGGGCTTATCTGGAGACGACA 402
Db 364 GGAGAGATGAGCTTCCTAGCAACAAATGTGAATCGACCAAAAGGGATAGGCA 423
Qy 403 AAGCCAGAAAAGGGAGAACCAAGGGAAAGGGAG 438
Db 424 AGACAGAAAATAATCAGTCGAGAAAGGGAAAG 459
Db 424 AGACAGAAAATAATCAGTCGAGAAAGGGAAAG 459

RESULT 15
US-08-718-904-4
Sequence 4, Application US/08718904
; Sequence 4, Application US/08718904
; Patent No. 6037329
; GENERAL INFORMATION:
; APPLICANT: Baird, J. Andrew
; APPLICANT: Chandler, Lois Ann
; APPLICANT: Sosnowski, Barbara A.
; TITLE OF INVENTION: COMPOSITIONS CONTAINING NUCLEIC ACIDS AND LIGANDS FOR THERAPEUTIC USE
; NUMBER OF SEQUENCES: 128
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/718,904
; FILING DATE: 24-SEP-1996
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 6037329
; REGISTRATION NUMBER: 39,317
; REFERENCE/DOCKET NUMBER: 760100.41501
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 682-4900
; TELEFAX: (206) 682-6031
; SEQUENCE CHARACTERISTICS:
; LENGTH: 728 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: both
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 13..90
; OTHER INFORMATION: /product= "leader sequence-encoding DNA"
; PCT-US95-10973A-27
; OTHER INFORMATION: /product= "VEGFI89-encoding DNA"
; OTHER INFORMATION: /product= "VEGFB206-encoding DNA"

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i NAME/KEY: CDS
i LOCATION: 13..90
i OTHER INFORMATION: /product= leader sequence encoding DNA
US-08-718-904-4

Query Match      22..8%; Score 108..8; DB 3; Length 728;
Best Local Similarity 59..8%; Pred. No. 3..4e-26;
Matches 201; Conservative 0; Mismatches 132; Indels 3; Gaps 1;
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Db 127 GAAGGTGGAGTTATGGATGTCTATAGGCACTAGCCATGCCATGACCCCTG 186
Qy 163 GTGTACATTGCGAGATGAACCCCTAATGAAAGTGTCTATATTCAGTCATGTGTC 222
Db 187 GTGGACATTCFTCCAGGATACCCCTATGAGATCGATACTTCAGGCATCTGTGTC 246
Qy 223 CTTCCTGAGTCGCTGTAGTGGCTGCTGCTGACGGGCTGACTGTGTGGCTTAANG 282
Db 247 CCCCTGATGGATGGGGGCTGCTGCAATGACGGGGCTGGAGTGCCCACTGAG 306
Qy 283 ACACCCAACTCACTATGAGATCTTAAGATCCCCAATCGGATCCACATTCCPAC 342
Db 307 GAGTCCAACTCACCATGGATPATGGGATCAACCTCACCAGGAGCA -- -CTATA 363
Qy 343 GTGGAGATGAGCATCTCTCGGAGATGATCTGGGAATGGAGCCATTCTGGAGACGACA 402
Db 364 GGAGAGATGAGCTTCAGCAACAAATGTAATGAGACCAAGAGGATAGAGCA 423
Qy 403 AAGGCTAGAAGGAGAAAACCAAGGGAGAGGAG 438
Db 424 AGACAGAAAAAAATCACTTCTGAGGAAGGGAAAG 459

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Search completed: September 16, 2004, 21:28:03
 Job time : 65 secs

GenCore version 5.1.6
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Query Score	Match %	Length	DB ID	Description
OM nucleic - nucleic search, using sw model						
Run on:	September 16, 2004, 17:54:38 ; Search time 2305 Seconds					
	(without alignments)					
8969-470 Million cell updates/sec						
Title: US-10-071-370A-3	1	477	100.0	477	6 AR117110 Sequence	
Perfect score: 477	2	477	100.0	477	6 AR138153 Sequence	
Sequence: 1 atgctggccatgaagtgtt.....ctgaggaaaccacatgtga 477	3	475.4	99.7	665	10 RATPLGF	
	4	419.4	87.9	1370	10 MMP1GF	
	5	419.4	87.9	1580	10 MMP16	
	6	419.4	87.9	1674	10 BC016567	
	7	414	86.8	417	6 AR117109 Sequence	
Scoring table: IDENTITY_NUC	8	414	86.8	417	6 AR338152 Sequence	
Gapop 10.0 , Gapext 1.0	9	230.2	48.3	513	6 AR117114 Sequence	
Searched: 3470272 seqs, 21671516995 residues	10	230.2	48.3	513	6 AR338157 Sequence	
Total number of hits satisfying chosen parameters:	11	230.2	48.3	513	9 BT007182 Homo sapi	
Minimum DB seq length: 0	12	230.2	48.3	513	12 BT008273 Synthetic	
Maximum DB seq length: 20000000000	13	230.2	48.3	597	9 S72960 Homo sapi	
Post-processing: Minimum Match 0%	14	230.2	48.3	1744	9 BC007789 Homo sapi	
Maximum Match 100%	15	230.2	48.3	1759	9 BC001422 Homo sapi	
Listing first 45 summaries	16	230.2	48.3	1780	9 BC007255 Homo sapi	
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1: gb_ba:*	18	229.8	48.2	465	6 AR338154 Sequence	
2: gb_htg:*	19	213.6	44.8	1645	6 AB4411 PIGF gene s	
3: gb_in:*	20	213.6	44.8	1645	6 AX234464 Sequence	
4: gb_on:*	21	213.6	44.8	1645	6 AX587633 Sequence	
5: gb_ov:*	22	213.6	44.8	1645	6 AX743110 Sequence	
6: gb_dat:*	23	213.6	44.8	1645	9 HSPLGF	
7: gb_ph:*	24	213.2	44.7	450	6 AR117115 Sequence	
8: gb_dl:*	25	213.2	44.7	450	6 AR338158 Sequence	
9: gb_pr:*	26	213.2	44.7	468	6 BD141689 Chimeric	
10: gb_ro:*	27	203.6	42.7	229131	2 AC114701 Rattus no	
11: gb_sts:*	28	203.6	42.7	248529	2 AC097592 Artificial	
12: gb_sy:*	29	195.6	41.0	1489	4 AB004272 Bos tauru	
13: gb_un:*	30	187.6	39.3	450	6 BD141690 Chimeric	
14: gb_vl:*	31	176.8	37.1	167700	2 AC079735 Mus muscu	
15: em_ba:*	c	32	176.8	37.1	2 AC127582 Mus muscu	
16: em_fun:*	33	147.4	30.9	474	6 BD141691 Chimeric	
17: em_hum:*	34	145.4	30.5	375	4 AY157708 Ovis arie	
18: em_in:*	35	129.2	27.1	390	12 ASPIGF	
19: em_mu:*	36	121.8	25.5	474	6 BD141692 Chimeric	
20: em_om:*	c	37	117	24.5	103010 9 AC004530 Homo sapi	
21: em_or:*	38	116.4	24.4	495	10 GPIVGEFA	
22: em_ov:*	39	112.8	23.6	645	4 CFA133758 Canis fam	
23: em_dat:*	40	110.8	23.2	654	4 AF133249 Canis fam	
24: em_ph:*	41	110.8	23.2	672	4 AF133250 Canis fam	
25: em_pl:*	42	109.4	22.9	715	5 AB011078 Gallus ga	
26: em_ro:*	43	108.8	22.8	677	6 AR272184 Sequence	
27: em_sts:*	44	108.8	22.8	728	6 AR272185 Sequence	
28: em_un:*	45	108.8	22.8	3747	6 AX780130 Sequence	

ALIGNMENTS

RESULT 1				
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	DEFINITION			
	ACCESSION	AR117110		
	VERSION	AR117110.1		
	KEYWORDS			
	SOURCE	Unknown.		
	ORGANISM	Unclassified.		
		1 (bases 1 to 477)		
REFERENCE				
AUTHORS		Bayne, M.L. and Thomas,K.A. Jr.		
TITLE		Vascular endothelial cell growth factor C subunit		
JOURNAL		US 6140073-A 38 31-OCT-2000;		
FEATURES		Location/Qualifiers		

Pred. No. is the number of results predicted by chance to have a

source	1..477	Score 477; DB 6; Length 477;	Qy	121	GAAGTGTGGGCCCAAGCTACTGCGGCCAATGGAGAACCTGGTGTACATTGGATGAA 180
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Query Match	100.0%	Pred. No. 5.1e-12;	Qy	181	CACCCATAATGAAAGTGCTCATATATTGTCGCTCATATTCAGTCGCATATGTCCTCTCAGTCGTGACT 240
Best Local Similarity	100.0%	Mismatches 0;	Db	181	CACCCATAATGAAAGTGCTCATATATTGTCGCTCATATTCAGTCGCATATTCAGTCGTGACT 240
Matches 477;	Conservative	Indels 0;	Gaps 0;		
Db	1 ATGCTGCCATGAAAGTGCTCATGTGCTTCTGAGGTCTAGTGGTTGGCTGTGAC 60		Qy	241	GGCTGCTCTGGTGCAGGCTGCTCATATTCAGTCGCATATTCAGTCGCATATTCAGTCGTGACT 300
Db	1 ATGCTGCCATGAAAGTGCTCATGTGCTTCTGAGGTCTAGTGGCTGTGAC 60		Db	241	GGCTGCTCTGGTGCAGGCTGCTCATATTCAGTCGCATATTCAGTCGTGACT 300
Qy	1 TCCCAGGGGCCCTGTCTGTGAAACAACTCAACAGAAATGGAAAGTGTGCCTTCAT 120		Qy	301	CAGTCCTTAAGATCCCCCATGGATTCACATGGATGACATTCTCT 360
Db	61 TCCCAGGGGCCCTGTCTGTGAAACAACTCAACAGAAATGGAAAGTGTGCCTTCAT 120		Db	301	CAGTCCTTAAGATCCCCCATGGATTCACATGGATGACATTCTCT 360
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Qy	121 GAAGTGTGGGCCAGACTGCGGCAATGGAAAGCTGGTGTACATTGGAGATGAA 180		Db	361	CAGGTGTAACCTGGAAATGGAAAGTGTGTGATTCATGGAGAACAGGAA 420
Db	121 GAAGTGTGGGCCAGACTGCGGCAATGGAAAGCTGGTGTACATTGGAGATGAA 180		Qy	421	ACCAAGGGAAAGGGAAAGGAAAGGAAACCCACCTGGAAACCCACCTGTGA 477
Qy	181 CACCCATAATGAAAGTGCTCATATTCAGTCGCATGTGCTTCTGAGTCGTGACT 240		Db	421	ACCAAGGGAAAGGGAAAGGAAAGGAAACCCACCTGGAAACCCACCTGTGA 477
Db	181 CACCCATAATGAAAGTGCTCATATTCAGTCGCATGTGCTTCTGAGTCGTGACT 240				
Qy	241 GGCTGCTCTGGTGCAGGAGSTCTGCACCTGGACGCTAAAGACAGCCAACATCACTATG 300	RESULT 3			
Db	241 GGCTGCTCTGGTGCAGGAGSTCTGCACCTGGACGCTAAAGACAGCCAACATCACTATG 300	RAPIGF	65 bp	mRNA	linear ROD 17-APR-1996
Qy	301 CAGTCCTTAAGATCCCCCATGGATTCACATGGATGACATTCTCT 360	LOCUS	Rattus norvegicus	placenta growth factor (PlGF) mRNA, complete cds.	
Db	301 CAGTCCTTAAGATCCCCCATGGATTCACATGGATGACATTCTCT 360	DEFINITION	Rattus norvegicus		
Qy	361 CAGGTGTAACCTGGAAAGGAAAGGAA 420	ACCESSION	L40030	GI: 1263413	
Db	361 CAGGTGTAACCTGGAAAGGAAAGGAA 420	VERSION	L40030.1		
Qy	421 ACCAAGGGAAAGGGAAAGGAAAGGAAACCCACCTGGAAACCCACCTGTGA 477	KEYWORDS	Rattus norvegicus (Norway rat)		
Db	421 ACCAAGGGAAAGGGAAAGGAAAGGAAACCCACCTGGAAACCCACCTGTGA 477	SOURCE	Rattus norvegicus		
Qy	AR338153 AR338153 Sequence 38 from patent US 656934-A 38-27-MAY-2003;	ORGANISM	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Murinae; Rattus.		
Db	AR338153 AR338153 Sequence 38 from patent US 656934-A 38-27-MAY-2003;	REFERENCE	1 (bases 1 to 65)		
Qy	Unknown.	AUTHORS	Disalvo, J., Bayne, M.L., Conn, G., Kwock, P.W., Trivedi, P.G., Soderman, D.D., Palisti, T.M., Sullivan, K.A. and Thomas, K.A.		
Db	Unknown.	TITLE	Purification and characterization of a naturally occurring vascular endothelial growth factor: placenta growth factor heterodimer		
Qy	Unknown.	JOURNAL	J. Biol. Chem. 270 (13), 7717-7723 (1995)		
Db	Unknown.	PUBLISHER	95221439		
Qy	Unknown.	COMMENT	Original source text: Rattus norvegicus cDNA to mENA.		
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Qy	Bayne, M.L. and Thomas, K.A., Jr.		/db_xref="taxon:10116"		
Db	Vascular endothelial cell growth factor C subunit		/cell_line="GS-9L"		
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Qy	Query Match 100.0% Score 477; DB 6; Length 477;		RSYCRMMLVYTADEPHNEVSHITSPSCULSRSGCCGDEGLIHCVALKTANITQI		
Db	Best Local Similarity 100.0% Pred. No. 5.1e-12;		LRKPPNRDPHYEMTSQDVLCRPLLETTKAERTRKSKRKOSKTPQTBEPLH		
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Qy	Gaps 0;				
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Qy	61 TCCCAGGGGCCCTGTGTGGAAACACTCAACAGAAATGGAAAGTGTGCCTTCAT 120				
Db	61 TCCCAGGGGCCCTGTGTGGAAACACTCAACAGAAATGGAAAGTGTGCCTTCAT 120				

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Qy 61 TCCAGGGGCCCTGTGCGGAAACACTCACAGAAATGGAAAGTGTGCCTTCAT 120	/db_xref="SWISS-PROT:P49764"
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Qy 121 GAAGTGTGGGCCAGCTACTGGGGCAATGGAGAGCTGGTGTACATGGAGATGA 180	gene
Db 160 GAAGTGTGGGCCAGCTACTGGGGCAATGGAGAGCTGGTGTACATGGAGATGA 219	polyA_site
Qy 181 CACCTTAATGAAGCTGTCTCATATAATTCTAGTCCCTCATGTCAGTCCTGTAGT 240	ORIGIN
Db 220 CACCTTAATGAAGCTGTCTCATATAATTCTAGTCCCTCATGTCAGTCCTGTAGT 279	Query Match 87.9%; Score 419.4; DB 1.0; Length 1370;
Qy 241 GGCTGCTGTGTGACAGGGCTGCACTGTGGCGCTAAAGACAGCCAACTCATATG 300	Best Local Similarity 92.5%; Pred. No. 1.1e-114;
Db 280 GGCTGCTGTGTGACAGGGCTGCACTGTGGCGCTAAAGACAGCCAACTCATATG 339	Matches 441; Conservative 0; Mismatches 36; Indels 0; Gaps 0;
Qy 301 CAGATCTTAAGATTCCTCCCAATCGGATTCACATCTTACGGAGATGACATTCCT 360	Qy 1 ATGCTGGCCATGAGCTGTCACTGTGGCTCTAGTGGCTCCTAGGTGCTGTGCT 60
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Qy 361 CAGATGTACTCTGCGAATGCAAGCTTCTGGAGACCAAAAGGGCAAAGGAGAAA 420	Qy 61 TCCCCAGGGGCCCTGTGCTGGAAACACTCAACAGAAATGGAAAGTGTGCTGCT 120
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Qy 421 ACCZAGGGAAAGGGAAAGCAAGGAAGAACCCACAGACTGAGAACCCCACCTGTGA 477	Qy 121 GAAGTGTGGGGCGCAGTACTGGGCCATGGAAAGTGTGCTGAGATGGAGATGA 180
Db 460 ACCZAGGGAAAGGGAAAGCAAGGAAGAACCCACAGACTGAGAACCCCACCTGTGA 516	Db 239 GAAGTGTGGGGTGGCAGTACTGTGCCATGGAAAGTGTGCTGAGATGGAGATGA 298
RESULT 4	Qy 241 GGCTGCTGTGGTGTGAGGGCTGCACTGTGGCGCTAAAGACAGCCAACTCATATG 300
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LOCUS	Qy 301 CAGATCTTAAGATTCCTCCCAATCGGATTCACATCTTACGGAGATGACATTCCT 360
DEFINITION	Db 419 CAGATCTGAAGATTCCTCCCAATCGGATTCACATCTTACGGAGATGACATTCCT 360
VERSION	Qy 361 CAGGATGTACTCTGCGAATGCAAGCTTCTGGAGACCAAAAGGGCAAAGGAGAAA 420
KEYWORDS	Db 479 CAGGATGTACTCTGCGAATGCAAGCTTCTGGAGACCAAAAGGGCAAAGGAGAAA 538
SOURCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; 1 (bases 1 to 1370) Mus musculus (house mouse)
ORGANISM	REFERENCE 421 ACCZAGGGAAAGGGAAAGCAAGGAACCCACAGACTGAGAACCCCACCTGTGA 477
REFERENCE	Db 539 ACCZAGGGAAAGGGAAAGCAAGGAACCCACAGACTGAGAACCCCACCTGTGA 595
AUTHORS	AUTHORS 1 Achen,M.G., Gad,J.M., Stacker,S.A. and Wilks,A.F.
TITLE	ARTICLE Placenta growth factor and vascular endothelial growth factor are co-expressed during early embryonic development 2 (bases 1 to 1580) Unpublished
JOURNAL	JOURNAL 2 Direct Submission 8903720 Placenta growth factor and vascular endothelial growth factor are co-expressed during early embryonic development
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REFERENCE	REFERENCE 2 (bases 1 to 1370) Unpublished
AUTHORS	AUTHORS 1 Achen,M.G., Gad,J.M., Stacker,S.A. and Wilks,A.F.
TITLE	ARTICLE Placenta growth factor and vascular endothelial growth factor are co-expressed during early embryonic development
JOURNAL	JOURNAL 2 Direct Submission Submitted (22-MAR-1996) M.G. Achen, Ludwig Institute for Cancer Genetics and Biophysics, Via G Marconi 12, 80125 Naples, ITALY Locality/Qualifiers 2 (bases 1 to 1580) Unpublished
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	Qy	301 CAGATCTAAAGATCCGCCAATGGATCCACATTCCTACCTGGAGATGACATTCT 360
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	Qy	361 CAGATGFACTCTGGATGAGCTGGCCATTCTGGAGAGACAACAGGGAAAGGAGAA 420
	Db	678 CAGATGFACTCTGGATGAGCTGGCCATTCTGGAGAGACAACAGGGAAAGGAGAA 737
	Qy	421 ACCAAGGGAAAGGAAAGGAAACCAAACCCAAAGGAGCTGAGACAGCTGAGA 477
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LOCUS		Mus musculus placental growth factor, mRNA (cDNA clone MGC:11495 IMAGE:2645771, complete cds.)
DEFINITION		Mus musculus placental growth factor, mRNA (cDNA clone MGC:11495 IMAGE:2645771, complete cds.)
ACCESSION	BC016567	
VERSION	1	GI:16741506
KEYWORDS		Mus musculus (house mouse)
SOURCE		Mus musculus
ORGANISM		Mus musculus (house mouse)
REFERENCE		Stratberg,R.L., Engold,E.A., Grouse,L.H., Derge,J.G., Schuler,G.D., Klausner,R.D., Collins,F.S., Wagner,L., Shemesh,C.M., Schaefer,C.F., Bhat,N.K., Altschul,S.F., Zeeberg,B., Burwitz,K.H., Schaefer,C.F., Moore,T., Max,S.I., Wang,J., Hsieh,F., Hopkins,R.F., Jordan,H., Jordan,H.,

Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.P., Bonaldo,M.J., Usdin,T.B., Toshiyuki,S.,	Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mulahay,S.A., Bosak,S.A., McEwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
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TITLE	Generation and initial analysis of more than 16,000 full-length human and mouse cDNA sequences
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
MEDLINE	2238857
PUBMED	12477332
REFERENCE	2 (bases 1 to 1674)
AUTHORS	Straubert,R.
TITLE	Direct Submission
JOURNAL	Submitted (31-OCT-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
REMARK	NIR-MGC Project URL: http://nrgc.nci.nih.gov
COMMENT	Contact: MGC help desk Email: cgapbs-r@mail.nih.gov
	Tissue Procurement: Lothar Hennighausen Ph.D.; Chu-Xia Deng Ph.D.
	CDNA Library Preparation: Life Technologies, Inc.
	CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIJNL)
	DNA Sequencing by: Baylor College of Medicine Human Genome Sequencing Center
	Center code: BCM-HGSC
	Web site: http://www.hgsc.bcm.tmc.edu/cdna/
	Contact: amg@bcm.tmc.edu
	Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulesged, H., Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Namavari, A.N., Gibbs, R.A.
	Clone distribution: MGC Clone distribution information can be found through the I.M.A.G.E. Consortium/LIJNL at: http://image.ljnl.gov
	Series: IRAK Plate: 16 Row: 3 Column: 3
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Qy 121 GAAGTGTGGGGCGAGCTACTGGGGCAATGGAGAGCTGGTGTACATGGAGATSA 180
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RESULT 8 AR338152

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

ORIGIN

Query Match 86.8%; Score 414; DB 6; Length 417;
 Best Local Similarity 100.0%; Pred. No. 4.3e-113;
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LOCUS

Sequence

36 from patent US 6569434.

AR338152

GI:33724884

Unknown.

Unclassified.

1 (bases 1 to 417)

Bayne, M.L. and Thomas, K.A. Jr.

Vascular endothelial cell growth factor C subunit

Patent: US 6569434-A 36 27-MAY-2003;

Location/Qualifiers

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Patent: US 6569434-A 36 27-MAY-2003;

Location/Qualifiers

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Location/Qualifiers

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Vascular endothelial cell growth factor C subunit

Patent: US 6569434-A 36 27-MAY-2003;

Location/Qualifiers

1..417

/organism="unknown"

/

tag). The CDS has been directionally cloned using BD In-Fusion(TM) cloning system between the Sali and HindIII sites of the PDNR-DUAL vector. Additional sequences in the clone: 'ACC' after Sali site and before 'ATG' to provide Kozak consensus sequence; 'GG' after last codon and before HindIII site to maintain reading frame.

Clone distribution: <http://bioinfo.clontech.com/orfclones>.

Location/Qualifiers

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- /clone_id="BD Creator (TM) CDS Library derived from MGC collection"
- /lab_host="BD Biosciences Clontech, 1020 East Meadow
- /lab_name="BD Biosciences Clontech, 1020 East Meadow Circle, Palo Alto, CA 94303, USA"
- /note="Vector: PDNR-Dual"
- 1. .513 /codon_start=1 /product="placental growth factor, vascular endothelial growth factor-related protein"
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Best Local Similarity 71.6%; Pred. No. 7.4e-58;
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Qy 61 TCC-----CAGGGGCCCTGCCAACGAGCTAACACAATGGAAGCT 108
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Qy 169 ATGGAGATGAAACCCCTATGAAAGTGTCTCATATAATTGCTGGCTCATCTCTG 228
Db 181 GTCGCTCCAGTACCCACGGAGTGGACATGTTGGCCATCTCTGTCTCCCTG 240

Qy 229 AGTCCTGTAGTGTGTCTGGTGTGAGGGCTGTGCTGGCTAAAGCACGCC 289
Db 241 CTGCGTCACCGGTCTGGCTGGCAATGAAATCTGCACTGTGGCTGGGCC 300

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FEATURES	source	SOURCE ORGANISM	synthetic construct artificial sequences.
REFERENCE AUTHORS		REFERENCE 1 (bases 1 to 513) Kalinine,N., Chen,X., Rolfs,A., Halleck,A., Hines,L., Eisenstein,S., Koundinya,M., Raphael,J., Moreira,D., Kelley,T., LaBaer,J., Lin,Y., Phelan,M. and Farmer,A.	Kalinine,N., Chan,X., Rolfs,A., Halleck,A., Hines,L., Eisenstein,S., Harvard Institute of Proteomics. Each CDS has been cloned in two forms: with and without stop-codon (to allow fusion with C-terminal tag). The CDS has been directionally cloned using BD In-Fusion(TM) cloning system between the Sali and HindIII sites of the PDNR-DUAL vector. Additional sequences in the clone: ACC, after Sali site and before 'ATG' to provide Kozak consensus sequence; 'GG' after last codon and before HindIII site to maintain reading frame.
TITLE	JOURNAL	JOURNAL	Submitted (13-MAY-2003) BD Biosciences Clontech, 1020 East Meadow Circle, Palo Alto, CA 94303, USA
COMMENT			This CDS clone is a part of a collection of human full length expression clones generated by BD Biosciences Clontech and the Harvard Institute of Proteomics. Each CDS has been cloned in two forms: with and without stop-codon (to allow fusion with C-terminal tag). The CDS has been directionally cloned using BD In-Fusion(TM) cloning system between the Sali and HindIII sites of the PDNR-DUAL vector. Additional sequences in the clone: ACC, after Sali site and before 'ATG' to provide Kozak consensus sequence; 'GG' after last codon and before HindIII site to maintain reading frame.
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 Sequencing Center (NISC),
 Gaithersburg, Maryland;
 web site: <http://www.nisc.nih.gov/>
 Contact: nisc_mgc@nigri.nih.gov
 Akter,N., Ayale,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
 Blakesley,R.W., Bouffard,G., Brein,K., Brinkley,C., Brooks,S.,
 Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haqnihi,P.,
 Hansen,N., Ho,S.-L., Karlins,E., Kuong,P., Larić,P., Legaspi,R.,
 Madiro, Q.L., Masiello,C., Maskeri,B., Mastrian,P.J., McCloskey,J.C.,
 McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
 Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
 Young,A., Zhang,L.-H. and Green,E.D.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Series: ITAL Plate: 20 Row: a Column: 15
 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 20149542.

Location/Qualifiers

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 - /mol_type="mRNA"
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 - 472..714
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misc_feature

ORIGIN

Query Match: 48..3%; Score: 230.2; DB: 9; Length: 1744;
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 Matches 336; Conservative 0; Mismatches 118; Indels 15; Gaps 2;

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 Db 325 ATGCCGGTCATGGCTGTCCTCCCTGCTTCCTGCGCTGGCTGCTGCC 384

Qy 61 TCC-----CAGGGGCCCTGAATGAAACTCAACAGAAATGAAAGTG 108
 Db 385 GCTGAGCCCCCAAGAGTGGCCCTGCTGAAACGCTCGTCAAGTGGAAAGTG 444

Db 109 GTGCCCTTCAATGAAAGTGTGGGCCAGGTTACTGCGGCCAATGAGAGCTGGTAC 168
 Db 445 GTACCCCTCCAGGAACGTGGCCCAAGCTACTGCGGCCGCTGAGGCTGGTAC 504

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 Db 505 GTCGTGTCCGGTAGCCCAAGGAGGTGGAGAACATGTCAGCCATCCCTGTC 564

Qy 229 AGTCGCTGTAGTGTGGCTGCTGGTACGGGGTCTGCACCTGTCAGCAC 288

Blakesley,R.W., Bouffard,G.G., Green,K., Brinkley,C., Brooks,S., Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Hagnighi,P., Hansen,N., Ho,S.-L., Karlin,S., Kwong,P., Lalic,P., Legaspy,R., Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D., McCloskey,J.C., McDowell,J., Pearson,R., Stantonpop,S., Thomas,P.J., Touchman,J.W., Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L., Young,A., Zhang,L.-H. and Green,E.D.

Clone distribution: MGC clone distribution information can be found through the T.M.A.G. Consortium/LINN at: <http://image.llnl.gov>
 Series: IRLA Plate: 4 Row: m Column: 6
 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 20149542.

FEATURES

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 /clone="MGC:1683 IMAGE:3139175"
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 1. .1759
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 341. .859
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CDS

434. .736
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 /db_xref="CD0:smart00141"

misc_feature

ORIGIN

Query Match Score 48.3%; Score 230.2; DB 9; Length 1759;
 Best Local Similarity 71.6%; Pred. No. 7.e-58; Gaps 2;
 Matches 336; Conservative 0; Mismatches 118; Indels 15; Gaps 2;
 Qy 1 ATGGTGGCATGAGCTGTACTCTGTTGAGGTCTAGTGGTGGCTGTGCAC 60
 Db 347 ATGCCGATGATGAGCTGTCTGCTGGAAACAATCAAGAAATTGGACTG 406
 Qy 61 TCC ----- CAGGGGGCTGTCTGCTGGAACTCAAGAAATTGGACTG 108
 Db 407 GCTTGCCCCAGCAATGGCTTGTGCTGGAACTGGCTGGAACTG 466
 Qy 109 GTGCGTTCAATGAGTGGGGCGCAGCTATGCCGCCATGGAAAGCTGTAC 168
 Db 467 GTACCCCTTCAGGAATGGGGCCGGAGCTACTGCCGGCTGGAGGGCTGTGCAC 526
 Qy 169 ATTCGAGATGAAACCCATTGAGTGGCTGCTCATATTCAGTCGGTGTGTCCTTG 228
 Db 527 GTCTGTGATGATGCCCTGGGGTGGAGCAATGTCAGCCCATCTGTGTCCTTG 596
 Qy 229 AGTGGCTTAGTGGCTGGTGGTGGACAGGGTGTGACTGTTGGCTTAAGACACC 288
 Db 587 CTGGCTGACCGSCTGTGGGGATGAAATCTGCTGTGCTGGAGACGCC 646
 Qy 289 AACATCACATGAGATCTAAAGATTCCCCAATCGGATCACATCCPACGTGGAG 348
 Db 647 AATGTCACATGAGCTCTAAAGAT--CCGTCGGACCGCCCTCACTGTGGAG 703

349 ATGACATTCTCTCAGGATGTACTCTGGAATGCGCTATTCTGGAGACAAAGGCA 408
 Db 704 CTGAGTCTCTGGCACCTGGCTCTGGATGGCTCTGGCC 763
 Qy 409 GAAGGAGAAAACCAAGGGAAAGGAGCAALANGCAAACCCCAAGA 457
 Db 764 GAAAGGAGAACCCAGGGCAAGGGAAAGGGAGGAGAAGGAGA 812

Search completed: September 16, 2004, 20:48:07
 Job time : 2308 secs

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OM nucleic - nucleic search, using sw mode!

Run on: September 16, 2004, 19:32:13 ; Search time 307 Seconds

(without alignments)
6600 .620 Million cell updates/sec

Title: US-10-071-370A-3
Perfect score: 477
Sequence: 1 atgtctggccatgaacctgtt.....ctgaggaaacccaccatgtca 477

Scoring table: IDENTITY_NUC
Gapop 10_0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters:

6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing First 45 summaries

N_Geneseq_29Jan04;*

1: geneseqn1980s;*

2: geneseqn1990s;*

3: geneseqn2000s;*

4: geneseqn2001s;*

5: geneseqn2001bs;*

6: geneseqn2002s;*

7: geneseqn2003as;*

8: geneseqn2003bs;*

9: geneseqn2003cs;*

10: geneseqn2004s;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	477	100.0	477	2	RAQ28956		Aaq28956 Sequence
2	477	100.0	477	3	RAZ39830		Aaz39830 VEGFB 158
3	477	100.0	477	4	RAC8315		Aac8315 Rat VEGF
4	477	100.0	477	8	ADA25600		Ada25600 Rat cDNA
5	475.4	99.7	477	2	RAO28952		Aaq28952 Sequence
6	475.4	99.7	477	2	RAQ23040		Aaq23040 Encodes V
7	475.4	99.7	477	2	RAV25538		Aav25538 Vascular
8	475.4	99.7	477	2	RAV25536		Aav25536 Vascular
9	475.4	99.7	477	4	RAF81273		Aaf81273 CDNA enco
10	475.4	99.7	477	4	RAF81272		Aaf81272 Rat VEGF
11	475.4	99.7	477	7	ACA62374		Aca62374 CDNA enco
12	475.4	99.7	477	7	ACA62371		Aca62371 CDNA enco
13	414	86.8	417	2	RAQ28955		Aaq28955 Sequence
14	414	86.8	417	3	RAZ39829		Aaz39829 VEGFB 138
15	414	86.8	417	4	RAK83514		Aac83514 Rat VEGF
16	414	86.8	417	8	ADA25598		Ada25598 Rat cDNA
17	412.4	86.5	417	2	RAQ23041		Aaq23041 Encodes V
18	412.4	86.5	417	4	RAV25537		Aav25537 Vascular
19	412.4	86.5	417	4	RAF81274		Aaf81274 CDNA enco
20	412.4	86.5	417	7	ACA62375		Aca62375 CDNA enco
21	412.4	86.5	417	7	ACA62372		Aca62372 CDNA enco
22	396.4	83.1	423	2	AAV25539		Aav25539 Vascular
23	230.2	48.3	513	3	Aaz39801		Aaz39801 Vascular

ALIGNMENTS

RESULT 1	
ID	AAQ28956 standard; cDNA; 477 BP.
XX	
AC	AAQ28956;
XX	
DT	25-MAR-2003 (revised)
DT	25-FEB-1993 (first entry)
XX	
XX	Sequence encoding vascular endothelial cell growth factor VEGF B 158
DE	DE amino acid residue subunit.
XX	Vascular development; mitogen; blood vessel;
KW	KW vascular endothelial growth factor; neovascularisation; ss.
XX	
OS	Rattus.
XX	
FH	Key
FT	CDS
FT	1 . .477 a
FT	/*tag=
XX	Location/Qualifiers
XX	EP506477-A1.
XX	EP506477-A1.
PD	30-SEP-1992.
XX	
PP	27-MAR-1992;
XX	
PR	28-MAR-1991;
XX	
PA	(MERCK & CO INC.
XX	
PI	Bayne ML, Thomas KA;
XX	
DR	WPI; 1992-325745/40.
DR	P-PSBB; AAR27337.
XX	
PT	Vascular endothelial cell growth factor sub-units - which stimulate vascular endothelial cell growth, used for inducing tissue repair and growth.
PT	
CC	The full length coding region of the B subunit or monomer of VEGF is determined from four sets of overlapping cDNA clones. Degenerate oligo primers based on the amino acid sequences from polypeptide L50 are used to PCR amplify the central region of the cDNA for VEGF AB, B monomer. A
CC	
CC	
PS	Disclosure; Fig 8; 61pp; English.
XX	

DT	26-FEB-2001	(first entry)	Qy	421 ACCAAGGGAAAGGAAAGCCAAAACCCACAGACTGAGGAACCCACCTGTGA 477
XX	Rat	VEGF subunit B coding sequence SEQ ID NO: 38.	Db	421 ACCAAGGGAAAGGAAAGCCAAAACCCACAGACTGAGGAACCCACCTGTGA 477
XX	vascular endothelial growth factor; VEGF C subunit; cell division;			
XX	KW	artificial blood vessel; tissue growth; tissue repair; ss.		
XX	Rattus sp.			
XX	US6140073-A.			
PN	DR	2001-014958/02.		
XX	P-PSDB; AAB-37508.			
XX	Human vascular endothelial cell growth factor (VEGF) C subunit DNA and			
PT	protein, useful for promoting vascular development and repair, and for			
PT	promoting tissue repair, especially for treating wounds in mammals.			
XX	Example 10; Fig 8; 58pp; English.			
PS	The present invention is concerned with the human vascular endothelial cell			
CC	growth factor (VEGF) C subunit. VEGF is a vascular endothelial cell			
CC	mitogen and can be used to promote vascular development and repair. The C			
CC	subunit may exist as a homodimer or a heterodimer with the VEGF A or B			
CC	subunit. VEGF can be used in the treatment of wounds of mammals, to cover			
CC	artificial blood vessels with vascular endothelial cells, in the			
CC	production of artificial blood vessels and to induce tissue repair or			
XX	growth.			
SQ	Sequence 477 BP; 123 A; 116 C; 133 G; 105 T; 0 U; 0 Other;			
Query Match	100.0%; Score 477; DB 4; Length 477;			
Best Local Similarity	100.0%; Pred. No. 4.1e-133;			
Matches	0; Mismatches 0; Indels 0; Gaps 0;			
XX	ATGCCTGGCCCTGAAAGCTGTCACTTGCTCTTGCAGGTCTAGCTGGTTGGCTGTGCCAC 60			
Qy	1 ATGCCTGGCCCTGAAAGCTGTCACTTGCTCTTGCAGGTCTAGCTGGTTGGCTGTGCCAC 60			
Db	1 ATGCCTGGCCCTGAAAGCTGTCACTTGCTCTTGCAGGTCTAGCTGGTTGGCTGTGCCAC 60			
Qy	61 TCCCAGGGGCCCTGCTGGAAACAACTCAAAGAAATGGAAAGTGTGCCCTTCAT 120			
Db	61 TCCCAGGGGCCCTGCTGGAAACAACTCAAAGAAATGGAAAGTGTGCCCTTCAT 120			
Qy	121 GAAAGTGTGCCCGCAGCTGACTGCCGCAATGGAAAGCTGGTTACATGGAGATGAA 180			
Db	121 GAAAGTGTGCCCGCAGCTGACTGCCGCAATGGAAAGCTGGTTACATGGAGATGAA 180			
Qy	181 CACCTTAATGAAAGTGTCAATATTCAGTCGGTCAATGTCCTCTGACTTCGCTGTAGT 240			
Db	181 CACCTTAATGAAAGTGTCAATATTCAGTCGGTCAATGTCCTCTGACTTCGCTGTAGT 240			
Qy	241 GGCTGTGTGTGACTGAGGGTCACTGACTGTGGCTTAAGACGCCAACATCACTATG 300			
Db	241 GGCTGTGTGTGACTGAGGGTCACTGACTGTGGCTTAAGACGCCAACATCACTATG 300			
Qy	301 CAGATCTTAAGATTCCCCCAATCGGGATTCACATTCAGTGGAGATGACATTCTCT 360			
Db	301 CAGATCTTAAGATTCCCCCAATCGGGATTCACATTCAGTGGAGATGACATTCTCT 360			
Qy	361 CAGGATGCTACTGCGAAATGGAGGCCCTATCTGGACAGCAGAAAGGAGGAGAA 420			
Db	361 CAGGATGCTACTGCGAAATGGAGGCCCTATCTGGACAGCAGAAAGGAGGAGAA 420			

RESULT 5	
Q28952	AAQ28952 standard; cdNA; 477 BP.
AAQ28952;	
25-MAR-2003	(revised)
25-FEB-1993	(first entry)
Sequence encoding vascular endothelial cell growth factor VEGF AB subunit B.	
Vascular development; mitogen; blood vessel; vascular endothelial growth factor; neovascularisation; ss.	
Homosapiens.	
Key	Location/Qualifiers
CDS	1..477 /*tag= a
EE506477-A1.	
30-SEP-1992.	
27-MAR-1992;	92EP-00302750.
28-MAR-1991;	91US-00676436.
(MERCK) MERCK & CO INC.	
Bayne ML, Thomas KA;	
WPI: 1992-335745/40.	
P-PSDB; AAR2353.	
Vascular endothelial cell growth factor sub-units - which stimulate vascular endothelial cell growth, used for inducing tissue repair and growth.	
Example; Fig 3; 61pp; English.	
GS-9L cells were cultured and the VEGF AB subunits were isolated and sequenced. The reduced and carboxymethylated protein eluted as two peaks at approx. 23 and 25 ml, that were of approx. equal area, as determined by monitoring absorbance at 210 nm. Samples of the two protein subunits isolated after reduction and carboxymethylation were each applied to polybrene-coated glass fiber filters and their N-terminal sequences were determined. The peak of absorbance eluting at approx 25 ml (A subunit) yielded an amino terminal sequence Ala Pro Thr Glu Gly Glu Gln Iys Ala His Glu Val Val identical to VEGF AA. The peak of absorbance eluting at approx. 23 ml (B subunit) yielded the N-terminal sequence Ala Leu Ser Ala	

QY	301 CAGATCTAAAGATTCCCCAATGGGATCCACATTCTTACGTGGAGATGACATTCT 360	QY	61 TCCCAAGGGGCCCTGCTGCTGGAAACAATCAACAGAAATGGAAAGTGGTGGCCCTTCAT 120
Db	301 CAGATCTAAAGATTCCCCAATGGGATCCACATTCTTACGTGGAGATGACATTCT 360	Db	61 TCCCAAGGGGCCCTGCTGCTGGAAACAATCAACAGAAATGGAAAGTGGTGGCCCTTCAT 120
QY	361 CAGGTGTTAATCTGGGAATCGGGCTTATCTGGAGAACAAANGGAGAAAGGAAA 420	QY	121 GAAGTGTGGGGCGGAGCTACTGGGGCAATGGAGAACCTGGTACATTGGAGATGAA 180
Db	361 CAGGTGTTAATCTGGGAATCGGGCTTATCTGGAGAACAAANGGAGAAAGGAAA 420	Db	121 GAAGTGTGGGGCGGAGCTACTGGGGCAATGGAGAACCTGGTACATTGGAGATGAA 180
QY	421 ACCAGGGAGAGGGAAAGCDAAAACCCACAGATCTGGAGAACCCACCTGTGA 477	QY	181 CACCCTAATGAAAGTGTCTCATATTICACTCCGTCATGTCCTGTTCTGAGTCGTGAST 240
Db	421 ACCAGGGAGAGGGAAAGCDAAAACCCACAGATCTGGAGAACCCACCTGTGA 477	Db	181 CACCTTAATGAAAGTGTCTCATATTICACTCCGTCATGTCCTGTTCTGAGTCGTGAST 240
RESULT 8		QY	241 GGCAGCTGGTGGAGGGTCTCACGTGTGGCTTAAGAACAGCCZACATCACTATG 300
AAV25536 standard; cDNA; 477 BP.		Db	241 GGCAGCTGGTGGAGGGTCTCACGTGTGGCTTAAGAACAGCCZACATCACTATG 300
XX	AAV25536;	QY	301 CAGACTTAAGATCCCTCAATTGGATCCACATTCTAGTGGAGATGACATTCT 360
AC		Db	301 CAGACTTAAGATCCCTCAATTGGATCCACATTCTAGTGGAGATGACATTCT 360
XX		QY	361 CAGGTGTTAATCTGGGAATCGGGCTTATCTGGAGAACAAANGGAGAAAGGAAA 420
DT	30-JUL-1998 (first entry)	Db	361 CAGGTGTTAATCTGGGAATCGGGCTTATCTGGAGAACAAANGGAGAAAGGAAA 420
XX		QY	421 ACCAGGGAGAGGGAAAGCDAAAACCCACAGATCTGGAGAACCCACCTGTGA 477
DE	Vascular endothelial growth factor I A subunit 3 encoding cDNA.	Db	421 ACCAGGGAGAGGGAAAGCDAAAACCCACAGATCTGGAGAACCCACCTGTGA 477
XX		QY	421 ACCAGGGAGAGGGAAAGCDAAAACCCACAGATCTGGAGAACCCACCTGTGA 477
KW	Vascular endothelial cell growth factor; VEGF II; rat; glioma cell; mitogenesis; blood vessel growth; artificial blood vessel; ss.	Db	421 ACCAGGGAGAGGGAAAGCDAAAACCCACAGATCTGGAGAACCCACCTGTGA 477
KW	Rattus sp.	OS	421 ACCAGGGAGAGGGAAAGCDAAAACCCACAGATCTGGAGAACCCACCTGTGA 477
XX		RESULT 9	
FH	Key	ID	AAF81273 standard; cDNA; 477 BP.
FT	CDS	XX	AAF81273;
FT	I .477	XX	AAF81273;
FT	/*tag= a	AC	AAF81273;
FT	/product= "VEGF I A subunit"	XX	
XX	US57267152-A.	XX	
PN		XX	23-NOV-2001 (first entry)
XX	PD 10-MAR-1998.	XX	
XX	PF 31-AUG-1994;	DE	CDNA encoding the mature 135 amino acid form of VEGF II B subunit.
XX	PR 21-SEP-1990;	XX	
XX	PR 05-JAN-1993;	XX	Rat; vascular endothelial growth factor II; VEGF-II; wound healing; vascular repair; neovascularisation; tissue repair; VEGF II B subunit; pulmonary; angiogenesis; ss.
PA	(MERI) MERCK & CO INC.	OS	
XX		XX	Rattus sp.
PT	Conn GL, Thomas KA, Bayne ML;	PX	
XX	WPI: 1998-206007/18.	PX	US6180107-B1.
DR	DR P-PSDB; AAW33644.	PD	30-JAN-2001.
XX		XX	98US-00038199.
PT	Vascular endothelial growth factor proteins - having specified A and B sub-units.	PF	10-MAR-1998;
PT		XX	
XX	Example 9; Fig 4; 46pp; English.	PR	21-SEP-1990;
PS		PR	05-JAN-1993;
XX	The present sequence encodes a rat vascular endothelial growth factor I (VEGF I) A subunit. The present invention comprising an A subunit from AAW5339, AAW5340 or AAW53641, and a B subunit from AAW53638, AAW53639 or the first 115-135 amino acids of AAW53638; and (2) a mammalian VEGF comprising a heterodimer or homodimer of B subunits. The growth factor is used for promoting vascular development and repair and for promoting tissue repair	XX	93US-00000834.
CC		PR	31-AUG-1994;
CC	Sequence 477 BP; 124 A; 116 C; 132 G; 105 T; 0 U; 0 Other;	XX	94US-00299185.
CC		XX	(MERI) MERCK & CO INC.
CC	Query Match 99.7%; Score 475.4; DB 2; Length 477;	XX	Stimulating angiogenesis or both, comprises administering mammalian vascular
CC	Best Local Similarity 99.8%; Pred. No. 1 2e-132;	XX	PT neovascularization or both, comprises administering two different subunits.
CC	Matches 476; Conservative 0; Mismatches 1;	XX	PT endothelial growth factor II comprising a
SQ	1 ATGCTGGCCATGAAGCTGTTACTGTGGCTTGAGCTGCTGGTGGCTGACAC 60	XX	CC The invention relates to a method for stimulating angiogenesis or wound
Qy	1 ATGCTGGCCATGAAGCTGTTACTGTGGCTTGAGCTGCTGGTGGCTGACAC 60	PS	CC healing through vascular repair, neovascularisation or both. The method
Db	1 ATGCTGGCCATGAAGCTGTTACTGTGGCTTGAGCTGCTGGTGGCTGACAC 60	XX	CC comprises administering to a patient a pharmaceutically effective amount
		XX	CC of mammalian vascular endothelial growth factor II (VEGF-II) comprising a
		XX	CC heterodimer of subunits A and B, or a homodimer of B subunits. VEGF-II is

CC useful for vascular development and repair; promotion of tissue repair,
 CC and the production of artificial vessels. The present sequence encodes
 CC the mature 135 amino acid form of VEGF II B subunit
 XX SQ Sequence 477 BP; 124 A; 116 C; 132 G; 105 T; 0 U; 0 Other;
 Query Match Best Local Similarity 99.7%; Score 475.4; DB 4; Length 477;
 Matches 476; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 ATGCTGGCATGAAGCTGTACTCTGCCTGTTGAGGCTTCACTGGCTGGTGCAC 60
 Db 1 ATGCTGGCATGAAGCTGTACTCTGCCTGTTGAGGCTTCACTGGCTGGTGCAC 60
 QY 61 TCCAGGGGCCCTGTCCTGGAAACACTCAACAGAAATGGAAAGTGCTGCCTTCAT 120
 Db 61 TCCAGGGGCCCTGTCCTGGAAACACTCAACAGAAATGGAAAGTGCTGCCTTCAT 120
 QY 121 GAAGTGGGGCGCAGCTAATGCCGAAATGGAAAGCTGCTGAGATGAA 180
 Db 121 GAAGTGGGGCGCAGCTAATGCCGAAATGGAAAGCTGCTGAGATGAA 180
 QY 181 CACCTTAATGCTGTCATATATTCACTCCGTCATGTCCTTCGAGTCCTGTTAGT 240
 Db 181 CACCTTAATGCTGTCATATATTCACTCCGTCATGTCCTTCGAGTCCTGTTAGT 240
 QY 241 GGCTGCTGTTGACGAGGGCTGTCACTATTCAGTCCTCCGTCATGTCCTGTTAGT 300
 Db 241 GGCTGCTGTTGACGAGGGCTGTCACTATTCAGTCCTCCGTCATGTCCTGTTAGT 300
 QY 301 CAGATCTTAAGATTCCCCAATGGGATCCACATTCTACGTTGGCTAAAGAGGCCAACATCACTATG 360
 Db 301 CAGATCTTAAGATTCCCCAATGGGATCCACATTCTACGTTGGCTAAAGAGGCCAACATCACTATG 360
 QY 361 CAGGATGTTCTGGAATGAGCCAAATGGGATCCACATTCTACGTTGGCTAAAGAGGCCAACATCACTATG 420
 Db 361 CAGGATGTTCTGGAATGAGCCAAATGGGATCCACATTCTACGTTGGCTAAAGAGGCCAACATCACTATG 420
 QY 421 ACCAGGGAAAGGAAAGGAAAGGAAACCCCAAGACTGAGGACCCACCTGTGA 477
 Db 421 ACCAGGGAAAGGAAAGGAAAGGAAACCCCAAGACTGAGGACCCACCTGTGA 477

RESULT 1.0
 ID AAF81272 standard; cDNA: 477 BP.
 XX AC AAF81272/
 XX DT 23-NOV-2001 (first entry)
 XX DE Rat VEGF I B subunit cDNA.
 XX KW Rat; vascular endothelial growth factor II; VEGF II; wound healing;
 KW vascular repair; neovascularisation; tissue repair; VEGF I B subunit;
 KW pulmonary; angiogenesis; ss.
 XX OS Rattus sp.
 XX PN US6180107-B1.
 XX PD 30-JAN-2001.
 XX PF 10-MAR-1998; 98US-00038199.
 XX PR 21-SEP-1990; 90US-00586638.
 PR 05-JUN-1993; 93US-00000834.
 PR 31-AUG-1994; 94US-00299185.
 XX (MERCK) MERCK & CO INC.
 XX PI Bayne ML, Conn GL, Thomas KA;

DR WPI: 2001-256064/26.
 P-PSDB; AAB73963.
 XX Stimulating angiogenesis or wound healing through vascular repair,
 PR neovascularization or both; comprises administering mammalian vascular
 PR endothelial growth factor II comprising two different subunits.
 XX Disclosure; Fig 4I-4K; 46pp; English.
 XX The invention relates to a method for stimulating angiogenesis or wound
 CC healing through vascular repair, neovascularisation or both. The method
 CC comprises administering to a patient pharmaceutically effective amount
 CC of mammalian vascular endothelial growth factor II (VEGF-II) comprising a
 CC heterodimer of subunits A and B, or a homodimer of B subunits. VEGF-II is
 CC useful for vascular development and repair, promotion of tissue repair,
 CC and the production of artificial vessels. The present sequence encodes
 CC VEGF I B subunit
 XX Sequence 477 BP; 124 A; 116 C; 132 G; 105 T; 0 U; 0 Other;
 Query Match 99.7%; Score 475.4; DB 4; Length 477;
 Best Local Similarity 99.8%; Pred. No. 1.2e-132;
 Matches 476; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 ATGCTGGCATGAAGCTGTACTCTGCCTGTTGAGGCTTCACTGGCTGGTGCAC 60
 Db 1 ATGCTGGCATGAAGCTGTACTCTGCCTGTTGAGGCTTCACTGGCTGGTGCAC 60
 QY 61 TCCAGGGGCCCTGTCCTGGAAACACTCAACAGAAATGGAAAGTGCTGCCTTCAT 120
 Db 61 TCCAGGGGCCCTGTCCTGGAAACACTCAACAGAAATGGAAAGTGCTGCCTTCAT 120
 QY 121 GAAGTGGGGCGCAGCTAATGCCGAAATGGAAAGCTGCTGAGATGAA 180
 Db 121 GAAGTGGGGCGCAGCTAATGCCGAAATGGAAAGCTGCTGAGATGAA 180
 QY 181 CACCTTAATGCTGTCATATATTCACTCCGTCATGTCCTTCGAGTCCTGTTAGT 240
 Db 181 CACCTTAATGCTGTCATATATTCACTCCGTCATGTCCTTCGAGTCCTGTTAGT 240
 QY 241 GGCTGCTGTTGACGAGGGCTGTCACTATTCAGTCCTCCGTCATGTCCTGTTAGT 300
 Db 241 GGCTGCTGTTGACGAGGGCTGTCACTATTCAGTCCTCCGTCATGTCCTGTTAGT 300
 QY 301 CAGATCTTAAGATTCCCCAATGGGATCCACATTCTACGTTGGCTAAAGAGGCCAACATCACTATG 360
 Db 301 CAGATCTTAAGATTCCCCAATGGGATCCACATTCTACGTTGGCTAAAGAGGCCAACATCACTATG 360
 QY 361 CAGGATGTTCTGGAATGAGCCAAATGGGATCCACATTCTACGTTGGCTAAAGAGGCCAACATCACTATG 420
 Db 361 CAGGATGTTCTGGAATGAGCCAAATGGGATCCACATTCTACGTTGGCTAAAGAGGCCAACATCACTATG 420
 QY 421 ACCAGGGAAAGGAAAGGAAAGGAAACCCCAAGACTGAGGACCCACCTGTGA 477
 Db 421 ACCAGGGAAAGGAAAGGAAAGGAAACCCCAAGACTGAGGACCCACCTGTGA 477

RESULT 11
 ID ACA62374
 XX DE CDNA encoding rat VEGF II B subunit.
 XX AC ACA62374;
 XX AC ACA62374;
 XX DT 19-ANG-2003 (first entry)
 XX ID ACA62374 standard; cDNA; 477 BP.

XX	Sequence 477 BP; 124 A; 116 C; 132 G; 105 T; 0 U; 0 Other;	DR	WPI: 1992-325745/40.
SQ	Query Match Score 99.7%; Score 475.4; DB 7; Length 477; Best Local Similarity 99.8%; Pred. No. 1.e-132; Matches 477; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	PR	Vascular endothelial cell growth factor sub-units - which stimulate vascular endothelial cell growth, used for inducing tissue repair and growth.
Qy	1 ATGTGGCATGAGCTTACTTGCTTCAAGTCAGCTGGTTGGTGTGCAC 60	XX	Disclosure; Fig 7; 61pp; English.
Db	1 ATGTGGCATGAGCTTACTTGCTTCAAGTCAGCTGGTTGGTGTGCAC 60	XX	The full length coding region of the B subunit or monomer of VEGF is determined from four sets of overlapping cDNA clones. Degenerate oligo primers based on the amino acid sequences from polypeptide L50 are used to PCR amplify the central region of the cDNA for VEGF AB, B monomer, A single band migrating at 108 bp was gel purified, digested with Sall, ligated into pGEM3zf (+) and sequenced. The nucleotide sequence obtained (pYG) was used to design antisense and sense PCR primers to amplify the 5' and 3' ends of the cDNA. These 5' and 3' clones are denoted p5V2 and p3V2 respectively. The entire base sequence for the 158 amino acid microheterogeneous B subunit and the 138 amino acid microheterogeneous B subunit are shown in AAQ28956 and AAQ28955. (Updated on 25-MAR-2003 to correct PN field.) (Updated on 25-MAR-2003 to correct PD field.)
Qy	61 TCCAGGGGCCCTCTGGAAACACTCACAGAAATGGAAAGTGGCTTCAAT 120	CC	Query Match Score 86.8%; Score 414; DB 2; Length 417; Best Local Similarity 100.0%; Pred. No. 3.4e-114; Mismatches 0; Indels 0; Gaps 0;
Db	61 TCCAGGGGCCCTCTGGAAACACTCACAGAAATGGAAAGTGGCTTCAAT 120	CC	Matches 414; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy	121 GAAGTGGGGCGGCAGCTA CTGCGGCCAATGAGCTGGTGATGGAGATAA 180	CC	QY 1 ATGCTGGCCATGAGCTTCACTTGAGGTTCTAGCTGGAGCTGGCTGGCAGC 60
Db	121 GAAGTGGGGCGCCAGCTA CTGCGGCCAATGAGCTGGTGATGGAGATAA 180	CC	Db 1 ATGCTGGCCATGAGCTTCACTTGAGGTTCTAGCTGGAGCTGGCTGGCAGC 60
Qy	181 CACCTTAATGAGTGTCTATATTCTGAGCTGGCTAACATCATG 240	CC	QY 61 TCCAGGGGCCCTGCTGGAAACACTCACAGAAATGGAAAGTGGATGGCTTCAAT 120
Db	181 CACCTTAATGAGTGTCTATATTCTGAGCTGGCTAACATCATG 240	CC	Db 61 TCCAGGGGCCCTGCTGGAAACACTCACAGAAATGGAAAGTGGCTTCAAT 120
Qy	241 GGCTGCTGTGTGAGCAGGGCTCTGACTCTGTCGGCTAACATG 300	CC	QY 121 GAAGTGTGGGGCCAGTACTGGCGCAATGGAGGCTGGTGATGGAGATAA 180
Db	241 GGCTGCTGTGTGAGCAGGGCTCTGACTCTGTCGGCTAACATG 300	CC	Db 121 GAAGTGTGGGGCCAGTACTGGCGCAATGGAGGCTGGTGATGGAGATAA 180
Qy	301 CAGATCTTAAGATGATTCCCCAAATGGGATTCACATTCTGAGGATGATTCT 360	CC	QY 181 CACCTTAATGAGTGTCTATATTCTGAGCTGGCTAACATCATG 240
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Qy	361 CAGATGTTACTCTGGAAATGGGCTTATCTGGAGACCAAGGGAGAAA 420	CC	QY 241 GGCTGCTGTGGGGCCAGTACTGGCGCAATGGAGGCTGGTGATGGAGATAA 180
Db	361 CAGATGTTACTCTGGAAATGGGCTTATCTGGAGACCAAGGGAGAAA 420	CC	Db 241 GGCTGCTGTGGGGCCAGTACTGGCGCAATGGAGGCTGGTGATGGAGATAA 180
Qy	421 ACCAGGGGAAGGAAAGAAAACCACAGACTTGAGGACCCACCTGTGA 477	CC	QY 301 CAGATCTTAAGATGATTCCCCAAATGGGATTCACATTCTGAGGAGATAA 180
Db	421 ACCAGGGGAAGGAAAGCAAAGCAACACCACAGACTTGAGGACCCACCTGTGA 477	CC	QY 361 CAGGATGTACTCTGGGAATGAGCTAACATGGAGGACCCACCTGTGA 414
RESUL	13	XX	Db 301 CAGATCTTAAGATGATTCCCCAAATGGGATTCACATTCTGAGGAGATAA 180
AAQ28955	AAQ28955 standard; CDNA; 417 BP.	XX	XX
ID	AAQ28955	XX	XX
XX		XX	XX
AC	AAQ28955;	XX	XX
XX		XX	XX
DT	25-MAR-2003 (revised)	XX	XX
DT	25-FEB-1993 (first entry)	XX	XX
XX		XX	XX
DB	Sequence encoding vascular endothelial cell growth factor VEGF B 138	XX	XX
DB	amino acid residue subunit.	XX	XX
XX	Vascular development; mitogen; blood vessel;	XX	XX
KW	vascular endothelial growth factor; neovascularisation; ss	XX	XX
XX	Rattus.	OS	OS
XX	Key	FH	RESULT 14
FT	CDS	FT	AAZ39829
FT		FT	ID AAZ39829 standard; CDNA; 417 BP.
XX		XX	XX
XX		XX	XX
PN	EP506477-A1.	AC	AZZ39829;
XX	30-SEP-1992.	XX	XX
PD		DT	15-FEB-2000 (first entry)
XX		XX	XX
PF	27-MAR-1992;	DB	VEGFB 138 amino acid residue subunit nucleotide sequence.
XX		XX	XX
PR	28-MAR-1991;	XX	VEGFB; vascular endothelial growth factor; B subunit; tissue growth; vascular development; artificial blood vessel; repair; human; ss.
XX		KW	KW
PA	(MERK) MERCK & CO INC.	XX	XX
XX	Bayne ML, Thomas KA;	OS	Homo sapiens.
PI		XX	XX
XX		FH	Key Location/Qualifiers
		1..417	
		/*tag= a	

FT CDS 1..417 /tag= a
FT /product= "VEGFB"
FT //note= "138 amino acid subunit"
XX US5994300-A.
PN XX 30-NOV-1999.
PD XX 20-SEP-1993; 93US-00124259.
PF XX 28-MAR-1991; 91US-00676436.
PR XX (MERI) MERCK & CO INC.
PA XX
P1 Thomas KA, Bayne ML;
XX WPI; 2000-038268/03.
DR P-PSDB; AAY5031.
XX Purified and isolated vascular endothelial cell growth factor C subunit
PT for the induction of tissue repair or growth.
XX Disclosure; Fig 7; 58pp; English.
CC This is the nucleotide sequence of a 138 amino acid residue B subunit of
CC vascular endothelial cell growth factor (VEGF). The invention relates to
CC a purified and isolated VEGF C subunit amino acid sequence AAY5702. VEGF
CC exists in various microheterogenous forms, and is useful for the
CC promotion of vascular development and repair. The invention also relates
CC to human VEGF heterodimers AC or BC, and homodimer CC, where A, B and C
CC are subunit amino acid sequences. The VEGF AC, BC or CC amino acid
CC sequences can be used in a tissue repairing pharmaceutical composition.
CC The novel growth factors are useful for the production or coverage of
CC artificial blood vessels with vascular endothelial cell. They are also
CC useful for the induction of tissue growth and repair.
XX Sequence 417 BP; 98 A; 100 C; 116 G; 103 T; 0 U; 0 Other;
SQ Query Match 86.8%; Score 414; DB 3; Length 417;
Best Local Similarity 100.0%; Pred. No. 3.4e-114;
Matches 414; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ANGCTGGCATGAAGCTTCACTTGCTTCTGGCTCCTACCTGGCTGGTGCAC 60
Db 1 ATGCTGGCATGAAGCTTCACTTGCTTCTGGCTCCTACCTGGCTGGTGCAC 60
Qy 61 TCCCCGGGCCCGCAGTACTGCCGGCAATGGAAACTCAACAGAAATGGAAAGCTGGCTTCAAT 120
Db 61 TCCCCGGGCCCGCAGTACTGCCGGCAATGGAAACTCAACAGAAATGGAAAGCTGGCTTCAAT 120
Qy 121 GAAGTGTGGCTGGCGCAATGGAAACTCAACAGAAATGGAAAGCTGGCTTCAAT 180
Db 121 GAAGTGTGGCTGGCGCAATGGAAACTCAACAGAAATGGAAAGCTGGCTTCAAT 180
Qy 181 CACCCATATGAAGTGTCAATATATTGTCGTCAATATATTGTCGTCAATATATTGTCGTCAAT 240
Db 181 CACCCATATGAAGTGTCAATATATTGTCGTCAATATATTGTCGTCAATATATTGTCGTCAAT 240
Qy 301 CAGATCTAAAGATTCCCCAATCCGAAATCCGAAATTCGAACTGTCGAGATGACATCT 360
Db 301 CAGATCTAAAGATTCCCCAATCCGAAATCCGAAATTCGAACTGTCGAGATGACATCT 360
Qy 361 CAGGATTACTCTGGATTCAGGCTTATCTGGAGACGACAAGGGAAAGGG 414
Db 361 CAGGATTACTCTGGATTCAGGCTTATCTGGAGACGACAAGGGAAAGGG 414
Qy AAC83514 standard; cDNA; 417 BP.
ID AAC83514
XX AC AAC83514;
XX DT 26-FEB-2001 (first entry)
XX DE Rat VEGF subunit B coding sequence SEQ ID NO: 36.
XX KW Vascular endothelial growth factor; VEGF C subunit; cell division;
XX artificial blood vessel; tissue growth; tissue repair; ss.
XX OS Rattus sp.
PN US6140073-A.
XX 31-OCT-2000.
PD XX 16-JAN-1996; 96US-00586039.
PF XX 28-MAR-1991; 91US-00676436.
PR XX 20-SEP-1993; 93US-00124259.
PA (MERI) MERCK & CO INC.
XX PI Thomas KA, Bayne ML;
XX WPI; 2001-014858/02.
DR DR P-PSDB; AAB37507.
XX Human vascular endothelial cell growth factor (VEGF) C subunit DNA and
PT protein, useful for promoting vascular development and repair, and for
PT promoting tissue repair, especially for treating wounds in mammals.
XX PS Example 10; Fig 7; 58pp; English.
XX The present invention is concerned with the human vascular endothelial
CC growth factor (VEGF) C subunit. VEGF is a vascular endothelial cell
CC mitogen and can be used to promote vascular development and repair. The C
CC subunit may exist as a homodimer or a heterodimer with the VEGF A or B
CC subunit. VEGF can be used in the treatment of wounds of mammals, to cover
CC artificial blood vessels with vascular endothelial cells, in the
CC production of artificial blood vessels and to induce tissue repair or
XX Sequence 417 BP; 98 A; 100 C; 116 G; 103 T; 0 U; 0 Other;
SQ Query Match 86.8%; Score 414; DB 4; Length 417;
Best Local Similarity 100.0%; Pred. No. 3.4e-114;
Matches 414; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ATCTGGGGCCCTGCTGGCTGGAAACTCAACAGAAATGGAAAGCTGGCTTCAAT 120
Db 1 ATGCTGGCCATAGCTGTTCACTGCTGGCTGGAAACTCAACAGAAATGGAAAGCTGGCTTCAAT 120
Qy 61 TCCCCGGGCCCGCAGTACTGCCGGCAATGGAAACTCAACAGAAATGGAAAGCTGGCTTCAAT 180
Db 61 TCCCCGGGCCCGCAGTACTGCCGGCAATGGAAACTCAACAGAAATGGAAAGCTGGCTTCAAT 180
Qy 121 GAAGTGTGGCTGGCGCAATGGAAACTCAACAGAAATGGAAAGCTGGCTTCAAT 180
Db 121 GAAGTGTGGCTGGCGCAATGGAAACTCAACAGAAATGGAAAGCTGGCTTCAAT 180
Qy 181 CACCCATATGAAGTGTCAATATATTGTCGTCAATATATTGTCGTCAATATATTGTCGTCAAT 240
Db 181 CACCCATATGAAGTGTCAATATATTGTCGTCAATATATTGTCGTCAATATATTGTCGTCAAT 240
Qy 301 CAGATCTAAAGATTCCCCAATCCGAAATCCGAAATTCGAACTGTCGAGATGACATCT 360
Db 301 CAGATCTAAAGATTCCCCAATCCGAAATCCGAAATTCGAACTGTCGAGATGACATCT 360
Qy 361 CAGGATTACTCTGGATTCAGGCTTATCTGGAGACGACAAGGGAAAGGG 414
Db 361 CAGGATTACTCTGGATTCAGGCTTATCTGGAGACGACAAGGGAAAGGG 414
Qy AAC83514 standard; cDNA; 417 BP.
ID AAC83514
XX AC AAC83514;
XX DT 26-FEB-2001 (first entry)
XX DE Rat VEGF subunit B coding sequence SEQ ID NO: 36.
XX KW Vascular endothelial growth factor; VEGF C subunit; cell division;
XX artificial blood vessel; tissue growth; tissue repair; ss.
XX OS Rattus sp.
PN US6140073-A.
XX 31-OCT-2000.
PD XX 16-JAN-1996; 96US-00586039.
PF XX 28-MAR-1991; 91US-00676436.
PR XX 20-SEP-1993; 93US-00124259.
PA (MERI) MERCK & CO INC.
XX PI Thomas KA, Bayne ML;
XX WPI; 2001-014858/02.
DR DR P-PSDB; AAB37507.
XX Human vascular endothelial cell growth factor (VEGF) C subunit DNA and
PT protein, useful for promoting vascular development and repair, and for
PT promoting tissue repair, especially for treating wounds in mammals.
XX PS Example 10; Fig 7; 58pp; English.
XX The present invention is concerned with the human vascular endothelial
CC growth factor (VEGF) C subunit. VEGF is a vascular endothelial cell
CC mitogen and can be used to promote vascular development and repair. The C
CC subunit may exist as a homodimer or a heterodimer with the VEGF A or B
CC subunit. VEGF can be used in the treatment of wounds of mammals, to cover
CC artificial blood vessels with vascular endothelial cells, in the
CC production of artificial blood vessels and to induce tissue repair or
XX Sequence 417 BP; 98 A; 100 C; 116 G; 103 T; 0 U; 0 Other;
SQ Query Match 86.8%; Score 414; DB 4; Length 417;
Best Local Similarity 100.0%; Pred. No. 3.4e-114;
Matches 414; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ATCTGGGGCCCTGCTGGCTGGAAACTCAACAGAAATGGAAAGCTGGCTTCAAT 120
Db 1 ATGCTGGCCATAGCTGTTCACTGCTGGCTGGAAACTCAACAGAAATGGAAAGCTGGCTTCAAT 120
Qy 61 TCCCCGGGCCCGCAGTACTGCCGGCAATGGAAACTCAACAGAAATGGAAAGCTGGCTTCAAT 180
Db 61 TCCCCGGGCCCGCAGTACTGCCGGCAATGGAAACTCAACAGAAATGGAAAGCTGGCTTCAAT 180
Qy 121 GAAGTGTGGCTGGCGCAATGGAAACTCAACAGAAATGGAAAGCTGGCTTCAAT 180
Db 121 GAAGTGTGGCTGGCGCAATGGAAACTCAACAGAAATGGAAAGCTGGCTTCAAT 180
Qy 181 CACCCATATGAAGTGTCAATATATTGTCGTCAATATATTGTCGTCAATATATTGTCGTCAAT 240
Db 181 CACCCATATGAAGTGTCAATATATTGTCGTCAATATATTGTCGTCAATATATTGTCGTCAAT 240
Qy 301 CAGATCTAAAGATTCCCCAATCCGAAATCCGAAATTCGAACTGTCGAGATGACATCT 360
Db 301 CAGATCTAAAGATTCCCCAATCCGAAATCCGAAATTCGAACTGTCGAGATGACATCT 360
Qy 361 CAGGATTACTCTGGATTCAGGCTTATCTGGAGACGACAAGGGAAAGGG 414
Db 361 CAGGATTACTCTGGATTCAGGCTTATCTGGAGACGACAAGGGAAAGGG 414
Qy AAC83514 standard; cDNA; 417 BP.
ID AAC83514
XX AC AAC83514;
XX DT 26-FEB-2001 (first entry)
XX DE Rat VEGF subunit B coding sequence SEQ ID NO: 36.
XX KW Vascular endothelial growth factor; VEGF C subunit; cell division;
XX artificial blood vessel; tissue growth; tissue repair; ss.
XX OS Rattus sp.
PN US6140073-A.
XX 31-OCT-2000.
PD XX 16-JAN-1996; 96US-00586039.
PF XX 28-MAR-1991; 91US-00676436.
PR XX 20-SEP-1993; 93US-00124259.
PA (MERI) MERCK & CO INC.
XX PI Thomas KA, Bayne ML;
XX WPI; 2001-014858/02.
DR DR P-PSDB; AAB37507.
XX Human vascular endothelial cell growth factor (VEGF) C subunit DNA and
PT protein, useful for promoting vascular development and repair, and for
PT promoting tissue repair, especially for treating wounds in mammals.
XX PS Example 10; Fig 7; 58pp; English.

Db	301	CAGATCTTAAGAATTCCCCCAATCGGGATCCACATTCTACGTGGAGATGACATTCTCT	360
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Db	361	CAGGATGTACTCTCGAAATGCAGGCCATTCTGGAGACGACAAGGCCAGAAAGG	414

Search completed: September 16, 2004, 20:53:23
Job time : 309 secs

Shet

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OM nucleic - nucleic search, using sw model

Run on: September 16, 2004, 20:53:28 ; Search time 348 Seconds
(without alignments)

6918.483 Million cell updates/sec

Title: US-10-071-370a-3

Perfect score: 477

Sequence: 1 atgtggccatgaaggctgtt.....ctgaggaaacccaccgtgta 477

Scoring table: IDENTITY NUC Gap0 10.0 , Gapext 1.0

Searched: 3327077 seqs, 2523723180 residues

Total number of hits satisfying chosen parameters: 6654154

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100%

Listing first 45 summaries

Database : Published Applications_NA:
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RESULT 1
 US-10-071-370a-3 ; Sequence 3, Application US/10071370A
 ; Publication No. US20030043471A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bayne, Marvin L.
 ; APPLICANT: Conn, Gregory L.
 ; APPLICANT: Thomas, Jr., Kenneth A.
 ; TITLE OF INVENTION: VASCULAR ENDOTHELIAL CELL GROWTH FACTOR
 ; TITLE OF INVENTION: II
 ; CURRENT APPLICATION NUMBER: US/10/071-370A
 ; PRIORITY APPLICATION NUMBER: 09/038,199
 ; PRIORITY FILING DATE: 1999-06-07
 ; PRIORITY APPLICATION NUMBER: 09/326,879
 ; PRIORITY FILING DATE: 2002-02-08
 ; PRIORITY APPLICATION NUMBER: 09/326,879
 ; PRIORITY FILING DATE: 1998-03-10
 ; PRIORITY APPLICATION NUMBER: 08/299,185
 ; PRIORITY FILING DATE: 1994-08-31
 ; PRIORITY APPLICATION NUMBER: 08/000,834
 ; PRIORITY FILING DATE: 1993-01-05
 ; PRIORITY APPLICATION NUMBER: 07/586,638
 ; PRIORITY FILING DATE: 1990-09-21
 ; NUMBER OF SEQ ID: 29
 ; SEQ ID NO: 3
 ; LENGTH: 477
 ; TYPE: DNA
 ; ORGANISM: rat
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (1) . . . (477)
 ; US-10-071-370a-3

Query Match Score 477; DB 15; Length 477;
 Best Local Similarity 100.0%; Pred. No. 2.6e-156;
 Matches 477; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	477	100.0	477	15 US-10-071-370A-3	Sequence 3, Appli
2	414	86.8	417	15 US-10-071-370A-3	Sequence 5, Appli
3	213.6	44.8	1645	9 US-09-795-006A-114	Sequence 114, App
4	213.6	44.8	1645	13 US-10-211-462-114	Sequence 114, App
5	213.6	44.8	1645	15 US-10-262-538-27	Sequence 27, Appli
6	213.6	44.8	1645	15 US-10-007-926A-103	Sequence 103, App
7	213.6	44.8	1645	15 US-10-101-510-590	Sequence 590, App
8	213.6	44.8	1645	16 US-10-021-660-35	Sequence 35, Appli
9	213.2	44.7	468	13 US-10-343-825A-11	Sequence 11, Appli
10	187.6	39.3	450	13 US-10-343-825A-12	Sequence 12, Appli
11	168.4	35.3	475	10 US-09-918-1813	Sequence 1813, Ap
12	147.4	30.9	474	13 US-10-343-825A-13	Sequence 13, Appli
13	121.8	25.5	474	13 US-10-343-825A-14	Sequence 14, Appli
14	109	22.9	1104	10 US-09-832-355A-93	Sequence 93, Appli

Qy 1 ATGCTGGCATGAAGCTTCACTTGTTCTTCAGGTCTTAGCTGGTTGGTGTGAC 60
 Db 1 ATGCTGGCATGAAGCTTCACTTGTTCTTCAGGTCTTAGCTGGTTGGTGTGAC 60
 Qy 61 TCCAGGGGCCCTGTCAGGTGTTCACTTGTTCTTCAGGTCTTAGCTGGTTGGTGTGAC 120
 Db 61 TCCAGGGGCCCTGTCAGGTGTTCACTTGTTCTTCAGGTCTTAGCTGGTTGGTGTGAC 120
 Qy 121 GAAGTGTGGGCCAGCTACTCGGGCCAATGGAGAAGTGTACATTGCGATGAA 180
 Db 121 GAAGTGTGGGCCAGCTACTCGGGCCAATGGAGAAGTGTACATTGCGATGAA 180
 Qy 181 CACCTTAATGAACTGGTCTATATACTCCGTCACTGTCAGTCCTGTAGT 240
 Db 181 CACCTTAATGAACTGGTCTATATACTCCGTCACTGTCAGTCCTGTAGT 240
 Qy 241 GGCTGCTGGGCCAGCTACTCGGGCCAATGGAGAAGTGTACATTGCGATGAA 300
 Db 241 GGCTGCTGGGCCAGCTACTCGGGCCAATGGAGAAGTGTACATTGCGATGAA 300
 Qy 301 CAGATCTAAAGATCCCCCATTGGATCACATTCTACGGGATGACATTCT 360
 Db 301 CAGATCTAAAGATCCCCCATTGGATCACATTCTACGGGATGACATTCT 360
 Qy 361 CAGATGACTCTGGAATGCCATTGGGATGACATTCTACGGGATGACATTCT 360
 Db 361 CAGATGACTCTGGAATGCCATTGGGATGACATTCTACGGGATGACATTCT 360
 Qy 421 ACCAGGGAAAGGAAAGAAAACCCCAAGGCAAAAGGCAAAAGGAGAAA 420
 Db 421 ACCAGGGAAAGGAAAGAAAACCCCAAGGCAAAAGGCAAAAGGAGAAA 420

RESULT 3
 US-09-795-006A-114
 ; Sequence 114, Application US/09795006A
 ; Patent No. US20020151680A1.

; GENERAL INFORMATION:
 ; APPLICANT: Alitalo et al.
 ; TITLE OF INVENTION: MATERIALS AND METHODS INVOLVING HYBRID VASCULAR
 ; TISSUE ENGINEERING: ENDOTHELIAL GROWTH FACTOR DNAs AND PROTEINS
 ; CURRENT APPLICATION NUMBER: US/09/795,006A
 ; CURRENT FILING DATE: 2001-02-26
 ; PRIORITY NUMBER: US 60/205,331
 ; PRIORITY FILING DATE: 2000-05-18
 ; PRIORITY NUMBER: US 60/185,205
 ; PRIORITY FILING DATE: 2000-02-25
 ; NUMBER OF SEQ ID NOS: 175
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 114
 ; LENGTH: 1645
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (32) .. (768)
 ; PRIORITY NUMBER: (32) .. (768)
 ; PRIORITY FILING DATE: 2000-05-18
 ; PRIORITY NUMBER: US 60/205,331
 ; PRIORITY FILING DATE: 2000-02-25
 ; PRIORITY NUMBER: US 60/185,205
 ; PRIORITY FILING DATE: 2000-02-25
 ; PRIORITY NUMBER: (32) .. (768)
 ; PRIORITY FILING DATE: 2000-05-18
 ; PRIORITY NUMBER: US 60/205,331
 ; PRIORITY FILING DATE: 2000-02-25
 ; PRIORITY NUMBER: US 60/185,205
 ; PRIORITY FILING DATE: 2000-02-25
 ; PRIORITY NUMBER: (32) .. (768)
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 ; PRIORITY NUMBER: US 60/185,205
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 ; PRIORITY NUMBER: US 60/185,205
 ; PRIORITY FILING DATE: 2000-02-25
 ; PRIORITY NUMBER: (32) .. (768)

Query Match 44.8%; Score 213.6; DB 9; Length 1645;
 Best Local Similarity 68.3%; Pred. No. 1..1e-63;
 Matches 332; Conservative 0; Mismatches 139; Indels 15; Gaps 2;

Qy 1 ATGCTGGCATGAAGCTTCACTTGTTCTTCAGGTCTTAGCTGGGCTGGAC 60
 Db 322 ATGCGGGCTATGAGCTGGGCTGGCTCTGGCTCTGGCTCTGGCTGCCT 381
 Qy 61 TCC-----CAGGGGCCCTGAGCTGGGCTAGCTGGCTCTGGCTCTGGCTGCAC 60
 Db 382 GCTGGCTCCACAGGGCTGGCTCTGGCTCTGGCTCTGGCTCTGGCTGCAC 441
 Qy 109 GTGGCTTCAATGAAAGTGTGGGCCAGTACTGGCTCTGGCTCTGGCTCTGGTAC 168
 Db 442 GTACCCCTCAGGAGTGTGGCTCTGGCTCTGGCTCTGGCTCTGGTAC 501
 Qy 169 ATTGGAGATGAAACCCCTAATGAGTGTCTCATATTCTGTCCTCATCTGTCCTCTG 228
 Db 502 GTCGTGTGGCTCCAGTACCCAGGAGTGTGGCTCTGGCTCTGGTAC 561

Query Match 86.8%; Score 414; DB 15; Length 417;
 Best Local Similarity 100.0%; Pred. No. 3e-134;
 Matches 414; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGCTGGCATGAAGCTTCACTTGTTCTTCAGGTCTTAGCTGGCTGGTGTGAC 60

Publication No. US20030152926A1
 GENERAL INFORMATION:
 APPLICANT: Murray, Richard
 APPLICANT: Glynn, Richard
 APPLICANT: Watson, Susan R.
 APPLICANT: EOS Biotechnology, Inc.
 TITLE OF INVENTION: No. US20030152926A1el Methods of Diagnosis of Angiogenesis, Compositions and Methods of Screening for Angiogenesis
 TITLE OF INVENTION: Modulators
 TITLE OF INVENTION: Filtration Reference: 018501-000710US
 CURRENT APPLICATION NUMBER: US/10/021,660
 CURRENT FILING DATE: 2001-12-06
 PRIORITY NUMBER: US/09/784,356
 PRIORITY FILING DATE: 2001-02-14
 PRIOR APPLICATION NUMBER: US/09/637,977
 PRIOR FILING DATE: 2000-08-11
 NUMBER OF SEQ ID NOS: 135
 SOFTWARE: FastSEQ for Windows Version 3.0
 SEQ ID NO: 35
 LENGTH: 1645
 TYPE: DNA
 ORGANISM: Homo sapiens
 US-10-021-660-35

Query Match 44.8%; Score 213.6; DB 15; Length 1645;
 Best Local Similarity 68.3%; Pred. No. 1.1e-63;
 Matches 332; Conservative 0; Mismatches 139; Indels 15; Gaps 2;

QY 1 ATGTCGGCCATGAAGCTGTACTCTGGCTTCTAGCTGGTTGGCTGTGCAC 60
 DB 322 ATGCCGGTCTATGAGCTCTGCTCCCTGCTCGAGCTCTGGCCCTGCCT 381
 QY 61 TCC-----CAGGGGCCCTGCTGCTGGAAACACTAACAAATGAACTG 108
 DB 382 GCTGTGCCCTCCAGTGCGCTTGCTGCTGGAAACGGCTGCTGGAAGTG 441
 QY 109 GTGCCTTTCAATGAGTGTGGGGCGCACTACTGCCGCAATTGGAGCTGTAC 168
 DB 442 GTACCCCTTCAGGAGTGGGGGGCGAGCTACTGCCGCAATTGGAGCTGTAC 168
 DB 442 GTACCCCTTCAGGAGTGGGGGGCGAGCTACTGCCGCAATTGGAGCTGTAC 501
 QY 169 ATTCGAGTAGAACCCCTTAATGAGTTCTCATATATTCTAGTCGGTCAATGTCGGTCTCTG 228
 DB 502 GTCTCGTCCGAGTACCCAGCGAGCTGGAGCACATGTTGCGCCATCCCTGCTCCCTG 561
 QY 229 AGTCGCTGTAGTGGGTGCTGGTACGAGGGCTGCACTGTGGCGCTAAAGACGCC 288
 DB 562 CTGGCTGCAACGGCTGCTGGGGAGATGAAATCTGCAGTGTGGCGACTGGGAGCGGCC 621
 QY 289 AACATCACTATGAGATCTAAAGATCTAACATCTCAATGCTGGAG 348
 DB 622 AATGTCACCTGAGCTCTAAAGAT---CCGTTCTGGAGCCGGCTCTAGTGGAG 678
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 DB 679 CTGACGTCTCCTACACGGTCTGGCTGCAATGTCGGCCCTCTGGGGAGAGATAAGCCG 738
 QY 409 GAAAGGAGAAACCAAGGGAAAGGGAAACCAANGCAAACCCACAGACTGGAAACCC 468
 DB 739 GAAAGGAGGGATGCTGTTCCCGGAGGTAACCCACCTGGAGGAGAACCCG 798
 QY 469 CACCTG 474
 DB 799 CACCCG 804

RESULT 9
 US-10-343-825A-11
 ; Sequence 11: Application US/10343825A
 ; Publication No. US2003003841A1
 GENERAL INFORMATION:
 ; APPLICANT: SHIBUYA, Masabumi
 ; TITLE OF INVENTION: Chimeric Human-Type Vascular Endothelial Cell Growth Factor
 ; FILE REFERENCE: P23303

CURRENT APPLICATION NUMBER: US/10/343,825A
 CURRENT FILING DATE: 2003-09-09
 PRIORITY NUMBER: PCT/JP01/06856
 PRIORITY FILING DATE: 2001-08-09
 NUMBER OF SEQ ID NOS: 15
 SOFTWARE: PatentIn version 3.2
 SEQ ID NO: 11
 LENGTH: 668
 TYPE: DNA
 ORGANISM: Artificial
 FEATURE:
 OTHER INFORMATION: Sequence encoding Chimeric VEGF protein
 US-10-343-825A-11

Query Match 44.7%; Score 213.2; DB 13; Length 468;
 Best Local Similarity 72.4%; Pred. No. 8.2e-64;
 Matches 310; Conservative 0; Mismatches 103; Indels 15; Gaps 2;

QY 1 ATGCTGGCCATGAGCTGTACTCTGGCTTCTAGTGGTTGGCTGTGCAC 60
 DB 1 ATGCCGGTCTATGAGCTGCTCCCTGCTCAGCTGCTGGCTGAAAT 60

QY 61 TCC-----CAGGGGCCCTGCTGCTGGAAACACTAACAAATGAACTG 108
 DB 61 GCCTGTGCCCTCCAGGAGTGGCTCTGGCTGAGGGTGAAGTGGACTG 120

QY 109 GTGCCTTTCAATGAGTGTGGGGCGCACTACTGCCGCAATTGGAGCTGTAC 168
 DB 121 GTACCCCTTCAGGAGTGTGGGGCGCTGGAGCTACTGCCGCACTACTGCCGCAATTGGAGCTGTAC 180

QY 169 ATTGAGATGAAACCTTAATGAGTGTGGCTCATATTTCTAGTCGGTCAATGTCGGTCTCTGCT 228
 DB 181 GTCGTGTCGGAGTACCCAGCGAGGTGAGCAATGCACTGCTGCTCCCTG 240

QY 229 AGTGGCTGTAGTGGCTGTGGCTGCTGGCTAAAGACAGCC 288
 DB 241 CTGGCTGCAACGGCTGCTGCTGGGGATGAAATCTGCACATGTCAGTGGCTGCGCCATCTGGAGAATCTGCAC 300

QY 289 AACATCACTATGAGATCTAAAGATCTAACATCTCAATGCTGGAG 348
 DB 301 ATGACATTCTCAGGCTCTAAAGAT---CCGTTCTGGAGCCCTCTAGTGGAG 357

QY 349 ATGACATTCTCAGGATGTACTCTGGGAATGCAAGGCCATTCTGGAGACAAAGCCA 408
 DB 358 CTGAGCTCTCTCAGACGCTGCTGGCTCTGGGGCTCTGGGGATGAAATCTGGAGAATGAGATGGCCG 417

DB 409 GAAAGGAG 416
 DB 418 GAAAGGTG 425

RESULT 10
 US-10-343-825A-12
 ; Sequence 12: Application US/10343825A
 ; Publication No. US2003003841A1
 GENERAL INFORMATION:
 ; APPLICANT: SHIBUYA, Masabumi
 ; TITLE OF INVENTION: Chimeric Human-Type Vascular Endothelial Cell Growth Factor
 ; FILE REFERENCE: P23103
 ; CURRENT APPLICATION NUMBER: US/10/343,825A
 ; PRIORITY NUMBER: PCT/JP01/06856
 ; PRIORITY FILING DATE: 2001-08-09
 ; NUMBER OF SEQ ID NOS: 15
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO: 12
 ; LENGTH: 450
 ; TYPE: DNA
 ; ORGANISM: Artificial
 ; FEATURE:
 ; OTHER INFORMATION: Sequence encoding Chimeric VEGF protein
 ; US-10-343-825A-12

Query Match 39.3%; Score 187.6; DB 13; Length 450;
 Best Local Similarity 68.7%; Pred. No. 7.6e-55;
 Matches 294; Conservative 0; Mismatches 119; Indels 15; Gaps 2;

Qy 1 ATGCTGGCATGAGCTGTGTCATCTGGGTTCTAGTGGTGTGAC 60
 Db 1 ATGCGGTCATGAGCTGTGTCCTGCTGAGCTCTGGGCTGCT 60
 Qy 61 TCC-----CAGGGGCCCTGTCTGGAAACAACAAATGAACTG 108
 Db 61 GCTGTGCCGCCAGAGGGCTTGCTGGAAAGGGTGTGAAGT 120
 Qy 109 GTGCCTTAATGAGTGTGGCCAGCTGCTGGTGAAGGTGTGAC 168
 Db 121 GTACCTTCAGGAGTGTGGCCAGCTGCAACCTGATACTGTGTTAT 180
 Qy 169 ATTCGAGATGAAACCCATTAAATGAAGTGTCTCATATTCAGTCGTCCTGGAAAGCTGTGCTTG 228
 Db 181 TTGGGAGAATAATCCAGAACACTAACCTAAATAATCCCCTGTGCTCCCTG 240
 Qy 229 AGTGGCTTAGTGGCTGTGACGGGGCTGCACTGTGGCTAAAGACACC 288
 Db 241 CTGGGTGCAACGGCTGTGGGATGGAATGTGCACTGTGGCTGGCC 300

RESULT 12
 US-10-343-825A-13

Qy 289 AACATCACATATGAGATCTAAAGTCCCCAAATCGGATCCAATTCCTACGTGGAG 348
 Db 301 AATGTCACCATGAGCTCTAAAGT--CCGGTCTGGGACCCGCCCTCCTACGTGGAG 357

Qy 349 ATGACATCTCTCAGGATGTACTCTGCCATATGCCAGACAAAGCCA 408
 Db 358 CTGAGCTCTCTGCACTGCACTGCTGCCATGTGGAGAAGATGAACCG 417

Qy 409 GAAGGGAG 416
 Db 418 GAAAGGTG 425

RESULT 11
 US-09-918-995-1813

Sequence 1813, Application US/09918995
 Publication No. US20030073623A1

GENERAL INFORMATION:
 APPLICANT: HYSEQ, Inc.
 TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
 FROM VARIOUS CDNA LIBRARIES
 FILE REFERENCE: 20411-756
 CURRENT APPLICATION NUMBER: US/09/918, 995
 CURRENT FILING DATE: 2001-07-30
 PRIOR FILING DATE: 1999-01-20
 NUMBER OF SEQ ID NOS: 38054
 SOFTWARE: FastSEQ for Windows Version 3.0
 SEQ ID NO: 1813
 LENGTH: 475
 TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: (1..(475))
 OTHER INFORMATION: n = A,T,C or G
 US-09-918-995-1813

Query Match 35.3%; Score 168.4; DB 10; Length 475;
 Best Local Similarity 66.0%; Pred. No. 4.2e-11;
 Matches 260; Conservative 0; Mismatches 131; Indels 3; Gaps 1;

Qy 81 TGGAAACACTCACAGAAATGAAAGTGGCTTCTCATGAAAGTGTGGGGCCACTA 140
 Db 29 TTGCTATCCCTCTCCAGGTGAAAGTGTGTTACCCCTTCCAGGAAGTGTGGGCACCTA 88

Qy 141 CTGGCGGGCAATGGAGAGCTGGGTGTAATTGGGATGAAACCCATTATGAAAGTGTCTCA 200
 Db 89 CTGGCGGGCGCTGGAGGGCTGGTGGAACTCCCGAGTACCTGCTGGGAGGCGAGGCGCA 148

Qy 201 TATATTCACTCCGTCATGTCCTCTGAGTCGTAGTGGCTGTGAGGAGGG 260
 Db 149 CATTTAGGCCACCTCTGTCAGTCCTGCGGCTGACGGGCTGTGAGA 208

Qy 261 TCTGCACTGTGTCGGCTAAAGACGCCACATCACTATGCAAGTCATTAAGATTCCTGGCTGACGGGCTGTGAGA 320
 Db 209 TCTGCACTGTGTCGGCTGGAGGCAATGTCACATGCAAGTCCTAAAGAT--CGG 265

Qy 321 CAATGGGATTCACATTCTACGGAGATGACATTCTCAGGATGFACTCTCGGAATG 380
 Db 266 GTCTGGGACCGGCCCTCTACAGGGAGCTGACCTTCCTCAGAACGTTGCTGGAAAG 325

Qy 381 CAGGCTTATTCTGGAGACAGAACAGGAGAAACAAAGGAGAAAGCCGAAGAGCA 440
 Db 326 CCAGCTCTGGCGGAGAGATGAGCCGGATGCTGTTCCCGGAGGTTA 385

Qy 441 AAGGAAAAACCCAAAGACTGAGAACCCACCTG 474
 Db 386 ACCACACCCTTGGAGGAGAACCCGACCCGACCCG 419

RESULT 13
 Sequence 13, Application US/10343825A
 Publication No. US20040038341A1

GENERAL INFORMATION:
 APPLICANT: SHIBUYA, Masabumi
 TITLE OF INVENTION: Chimeric Human-Type Vascular Endothelial Cell Growth Factor
 FILE REFERENCE: P2-303
 CURRENT APPLICATION NUMBER: US/10/343, 825A
 CURRENT FILING DATE: 2003-09-09
 PRIOR APPLICATION NUMBER: PCT/JP01/06856
 PRIOR FILING DATE: 2001-08-09
 NUMBER OF SEQ ID NOS: 15
 SOFTWARE: Patentin version 3.2
 SEQ ID NO: 13
 LENGTH: 474
 TYPE: DNA
 ORGANISM: Artificial
 FEATURE:
 OTHER INFORMATION: Sequence encoding Chimeric VEGF protein

US-10-343-825A-13

Query Match 30.9%; Score 147.4; DB 13;
 Best Local Similarity 70.1%; Pred. No. 9.7e-41;
 Matches 218; Conservative 0; Mismatches 81; Indels 12; Gaps 1;

Qy 1 ATGCTGGCATGAGCTGTTCACTGCTTCAGGCTCTACCTGGCTGGCTGGAC 60
 Db 1 ATGGGGTCTGGCTATGAGCTGTTCCCTGCTGGCTGGCTGGCTGGCT 60

Qy 109 GTCCTTCAATGAGTGGGGCAACTCTGGCCCATGGAAAGTGTGAC 108
 Db 61 GCTGTGCCCTGGCTATGAGCTGTTCCCTGCTGGCTGGCTGGCTGGCT 120

Qy 121 GTCACCTTCAGGAAAGTGGGGCCGAGCTGCTGGCTGGAGATGAAACAGA 180

Qy 169 ATTGAGTGAACCCCTAATGAGTGTCTATATTCAGTCGTCATGTCNCCTGTGCT 228

Db 181 GTCGTGTCGGAGTACCCCTGGGGCTGGCTGGCTGGCTGGCTCCCTG 240

Qy 229 ATGCGCTGCTGGCTGTGCTGGAGGAGGGCTGCACTGTGGGGCTAAAGACGCC 288

Db 241 CGCGCTGCACCGCTCTGCTGGAGATGAACTGTCAGGGTGAACAGA 300

Qy 289 AACATCACT 299

Db 301 AAATAAACTGT 311

RESULT 13
US-10-343-825A-14
; Sequence 14, Application US/10343825A
; Publication No. US2004038341A1
; GENERAL INFORMATION:
; APPLICANT: SHIBUYA, Masabumi
; TITLE OF INVENTION: Chimeric Human-Type Vascular Endothelial Cell Growth Factor
; FILE REFERENCE: P23303
; CURRENT APPLICATION NUMBER: US/10/343,825A
; CURRENT FILING DATE: 2003-09-09
; PRIOR APPLICATION NUMBER: PCT/JP01/06856
; PRIOR FILING DATE: 2001-08-09
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO: 14
; LENGTH: 474
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Sequence encoding ChimERIC VEGF protein
US-10-343-825A-14

Query Match Score 121.8; DB 13; Length 474;
Best Local Similarity 65.0%; Pred. No. 9.2e-32;
Matches 202; Conservative 0; Mismatches 97; Indels 12; Gaps 1;

Qy 1 ATGCGGGCATGAGCTGTACTTGCAGGTCCTAGGTGGTGGAC 60
Db 1 ATGCGGGCATGAGCTGTACTTGCAGGTCCTAGGTGGTGGAC 60
Qy 61 TCC-----CAGGGGGCTGTGCTCTGCTCTGAGCTCTGGAA 108
Db 61 GCTGNGCCCCAACAGAGTGCGGCTGTCGCTGGAAAGCTGAAGTC 120
Qy 109 GTGCCCTTCAATGAGTGGGGCGCAGCTACTGGCGGCAATGGAGCTGGTGTAC 168
Db 121 GTACCCCTTCAGGAAGTGGGGCGCAGCTACTGGCGGCAATGGAGCTGGTGTAC 180
Qy 169 ATTGGAGATAAACCCCTTAATGAACTGTCATATAATTGGCTCGTCAATGGTGTCTCTG 228
Db 181 TTGGGAGAAGATAATCAGAAAGACTAACATACATATACTGGCTCGTCAATGGTGTCTCTG 240
Qy 229 AGTCGCTGTAGTGGCTGGTGGTGAAGGCTGGCACTGTGGCTAAAGACGCC 288
Db 241 CTGCGCTGAGCCGGCTGGCGCATGAAATCGCACTGAACTGAGCTGTGAAACAASA 300
Qy 289 AACATCACTAT 299
Db 301 AATACAACTGT 311

RESULT 14
US-09-832-355A-93
; Sequence 93, Application US/09832355A
; Publication No. US20030027751A1
; GENERAL INFORMATION:
; APPLICANT: Kessler, Paul
; TITLE OF INVENTION: VEGF FUSION PROTEINS
; FILE REFERENCE: 205654
; CURRENT APPLICATION NUMBER: US/09/832,355A
; CURRENT FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 126
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO: 93
; LENGTH: 1104
; TYPE: DNA
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Synthetic
US-09-832-355A-93

Query Match Score 109; DB 10; Length 1104;
Best Local Similarity 58.1%; Pred. No. 4.2e-27;
Matches 212; Conservative 0; Mismatches 150; Indels 3; Gaps 1;

Qy 103 GAAGTGGCCCTTCAATGAACTGGGGCTGACTGCAGGCAATGGAGCTG 162
Db 115 GAAGTGGAACTGGTGAAGTCTGATGGTCTGATCAATCGAGACCTG 174
Qy 163 GTGTACATTGAGTGGCTGAGTGGCTGATGAGTGGCTGATGAGTGGCTG 222
Db 175 GTGACATCTTCAGGAACTCTGATGAGTGGATCATCTCAAGCCATCTG 234
Qy 223 CTTCTGAGTCGCTGTAGTGGCCTGCTGTGGTGAAGGGCTGACTGTGGCTAAAG 282
Db 235 CCCCTGATCGATCGGGCTGTGGTGAAGGGCTGAGTGTGGCOACTAG 294
Qy 283 ACAGCCAACTACATGAGATGAGATCTTAAAGATTCGAGATGGCTCTCT 342
Db 295 GAGTCACAACTACATCACCATGAGATTGGATCAAAACCTCACAAAGCCAGCA--CATATA 351
Qy 343 GTGGAGATAACATTCTAGGATGAGCTTGTGGAGAGCTTGTGGAGAGCA 402
Db 352 GGAGAGATGAGTGTCTACAGCAACAAATGGTGAAGGAGCAAAAGTAGAGCA 411
Qy 403 AAGGAGAAAGGGAAAACCAGGGAGAGCAAGGAAAGCAAGACTGAG 462
Db 412 AGACAGAAAATGTGACAGGCCAGGGATCATATGAGGACCATCAAAGACTGTGAG 471

RESULT 15
US-10-294-228-5
; Sequence 5, Application US/10294228
; Publication No. US2004018176A1
; GENERAL INFORMATION:
; APPLICANT: Tolentino, Michael J.
; APPLICANT: Reichl, Samuel Jordan
; TITLE OF INVENTION: Compositions and Methods for siRNA
; TITLE OF INVENTION: Inhibition of Angiogenesis
; FILE REFERENCE: 4382-6-1
; CURRENT APPLICATION NUMBER: US/10/294,228
; CURRENT FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: US 60/398,417
; PRIOR FILING DATE: 2002-07-24
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 5
; LENGTH: 670
; TYPE: DNA
; ORGANISM: Homo sapiens

Query Match Score 108.8; DB 16; Length 670;
Best Local Similarity 59.8%; Pred. No. 3.9e-27;
Matches 201; Conservative 0; Mismatches 132; Indels 3; Gaps 1;

Qy 103 GAAGTGGCCCTTCAATGAGTGGCTGAGGCGCAATGGAGAGCTG 162
Db 139 GTGGAAATCTTCAGGAACTCTGATGAGTGGCTCTGATGAGTGGCTAACTGAGCACTG 198
Qy 163 GTGTACATTGAGTGGCTGAGTGGCTGATGAGTGGCTGATGAGTGGCTAAAG 282
Db 199 CCCCTGATGGATGGCTGGGGCTGTGCAAATGACGGGGCTGGACTGTGGCCATCTGAGCTG 258
Qy 283 ACAGCCAACTACATCACCATGAGATCTTAAAGATGCCCAATCGGATCCACATCTC 342

Db	259	GAGTCCAAACATCACCATTGAGATTATGGGATCAAACTCACCAGGCAGCA	--CTATA 315
QY	343	GTGGAGATGACATTTCCTGGGATGTTCTGGGATGAACTCTGGGCTTATCTGGGAGACGACA	402
Db	316	CGAGAGATGAGCTTCCTAZGCRCAACAAATGTAATGACACAAAAGAGGATAGAGCA	375
QY	403	AAGGCCAGAAAGGAGCAAACCAAGGGGAAGAGGAAG	438
Db	376	AGACAGAAAAAATCAGTTCGGGAAAGGAAG	411

Search completed: September 16, 2004, 22:22:40
Job time : 350 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 13, 2004, 09:33:13 ; Search time 129 Seconds

(without alignments)
346.066 Million cell updates/sec

Title: US-10-071-370A-4

Perfect score: 846

Sequence: 1 MLAMKLFCTFLQLLAGLAVH.....RKTKGKRKQSKTPTQTEPHL 158

Scoring table: BLOSUM62

Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : A_Genesseq_29Jan04:
 1: genesseqP1980s: *
 2: genesseqP1990s: *
 3: genesseqP2000s: *
 4: genesseqP2001s: *
 5: genesseqP2002s: *
 6: genesseqP2003s: *
 7: genesseqP2003s: *
 8: genesseqP2004s: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	846	100.0	AAR27353	Aar27353 Sequence
2	846	100.0	AAR27357	Aar27357 Sequence
3	846	100.0	AAR22349	Aar22349 Rat VEGF-
4	846	100.0	AAW53644	AAw53644 Vascular
5	846	100.0	AAW53646	AAw53646 Vascular
6	846	100.0	AY57032	Aay57032 VEGFP 158
7	846	100.0	AAB37508	Aab37508 Rat VEGF
8	846	100.0	AAB71963	Aab71963 Rat VEGF
9	846	100.0	AAB71964	Aab71964 Rat VEGF
10	846	100.0	ABU62003	Abu62003 Amino aci
11	846	100.0	ABU62006	Abu62006 Amino aci
12	846	100.0	ADA25601	Ada5601 Rat VEGF
13	740	87.5	AAR27356	Aar27356 Sequence
14	740	87.5	AAR22350	Aar22350 Rat VEGF-
15	740	87.5	AAW53645	AAw53645 Vascular
16	740	87.5	AY57031	Aay57031 VEGFB 138
17	740	87.5	AAB37507	Aab37507 Rat VEGF
18	740	87.5	AAB71966	Abu71966 Rat VEGF
19	740	87.5	ABU62004	Abu62004 Amino aci
20	740	87.5	ABU62007	Abu62007 Amino aci
21	740	87.5	ADA25599	Ada5599 Rat VEGF
22	729	86.2	AAB36347	Aab36347 Vascular
23	501.5	59.3	AY57025	Aay57025 Vascular
24	501.5	59.3	AAB37510	Aab37510 Human VEG
25	501.5	59.3	ADA25607	Ada25607 Rat VEGF

ALIGNMENTS

RESULT 1
ID AAR27353 standard; protein; 158 AA.

XX	AC	AAR27353;
XX	DT	25-MAR-2003 (revised)
DT	DT	25-FEB-1993 (first entry)
XX	DE	Sequence of vascular endothelial cell growth factor VEGF AB subunit B.
XX	KW	Vascular development; mitogen; blood vessel; neovascularisation.
XX	OS	Homo sapiens.
XX	XX	Location/Qualifiers
FT	FT	Modified-site 97
XX	XX	/label= glycosylation site
XX	PN	EP06471-A1.
XX	PD	30-SEP-1992.
XX	PF	27-MAR-1992;
XX	PR	28-MAR-1991;
XX	XX	911US-00676436.
XX	PA	(MERCK & CO INC.
XX	PI	Bayne ML, Thomas KA;
XX	DR	WP1; 1992-32574/40.
XX	DR	N-FSDB; AAQ28952.
XX	PT	Vascular endothelial cell growth factor sub-units - which stimulate vascular endothelial cell growth, used for inducing tissue repair and growth.
XX	PS	Example; Fig 3; 61pp; English.
XX	CC	GS-9L cells were cultured and the VEGF AB subunits were isolated and sequenced. The reduced and carboxymethylated protein eluted as two peaks at approx. 23 and 25 ml that were of approx. equal area as determined by monitoring absorbance at 210 nm. Samples of the two protein subunits isolated after reduction and carboxymethylation were each applied to polybrene-coated glass fiber filters and their N-terminal sequences were determined. The peak of absorbance eluting at approx 25 ml (A subunit)

CC Yielded an amino terminal sequence Ala Pro Thr Glu Gly Glu Gln Lys Ala
 CC His Glu Val Val identical to VEGF AA. The peak of absorbance eluting at
 CC approx. 23 ml (B subunit) yielded the N-terminal sequence Ala Leu Ser Ala
 CC Gly Asn Xaa Ser Thr Glu Met Val Val Pro Phe Asn Glu Val plus a nearly
 CC equal amount of a truncated form of the same sequence missing the first
 CC three residues. The missing X residue correspond to an Asn in the cloned
 CC sequence. The A and sum of the B chain peptides were recovered in nearly
 CC equal amounts supporting the interpretation that the two peptides
 CC combine to form an AB heterodimer in VEGF II. The form of VEGF mature
 CC A subunit in the heterodimer is the 164 amino acid form. The form of VEGF
 CC B mature B subunit in the heterodimer is the 135 amino acid form derived
 CC from the 158 full length amino acid form. (Updated on 25-MAR-2003 to
 CC correct PN field.) (Updated on 25-MAR-2003 to correct PD field.)

Sequence 158 AA;

```
Query Match 100.0%; Score 846; DB 2; Length 158;
Best Local Similarity 100.0%; Pred. No. 4e-86;
Matches 158; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

Qy 1 MIAAMKLFICFLQVLAGIHLVSGALSAGNNSTEMEVVYGRSVCGRPMKLVYTADE 60
Db 1 MIAAMKLFICFLQVLAGIHLVSGALSAGNNSTEMEVVYGRSVCGRPMKLVYTADE 60
Qy 61 HPNEVSHIFSPSCVLLSRSQGCGDGEGLHCVALKTANTMQILKIPPRDPHSYVENTFS 120
Db 61 HPNEVSHIFSPSCVLLSRSQGCGDGEGLHCVALKTANTMQILKIPPRDPHSYVENTFS 120
Qy 121 QDVLCERPILETTKAERRKTKGKRKQSKTPOTEPEHL 158
Db 121 QDVLCERPILETTKAERRKTKGKRKQSKTPOTEPEHL 158

RESULT 2

AAR27357
ID AAR27357 standard; protein; 158 AA.
XX AC
AC AAR27357;

XX DT 25-MAR-2003 (revised)
DT 25-FEB-1993 (first entry)

XX Sequence of vascular endothelial cell growth factor VEGF B 158 amino acid
 DE residue subunit.

XX

KW vascular development; mitogen; blood vessel;
 KW vascular endothelial growth factor; neovascularisation.

XX OS Rattus.

XX PR EP506477-A1.

XX PD 30-SEP-1992.

XX PF 27-MAR-1992; 92EP-00302750.

XX PR 28-MAR-1991; 91US-00676436.

XX DR WPI; 1992-325745/40.

XX PA (MERCK & CO INC.

XX XX Bayne ML, Thomas KA;

XX PR N-PSDB; AAQ28956.

XX PR Vascular endothelial cell growth factor sub-units - which stimulate
 PR vascular endothelial cell growth, used for inducing tissue repair and
 PR growth.

XX PS Disclosure; Fig 8; 61pp; English.

XX The full length coding region of the B subunit or monomer of VEGF is
 CC determined from four sets of overlapping cDNA clones. Degenerate oligo.

CC primers based on the amino acid sequences from polypeptide L50 are used
 CC to PCR amplify the central region of the cDNA for VEGF AB, B monomer. A
 CC single band migrating at 108 bp was gel purified, digested with Sall,
 CC ligated into pGEM3Zf(-) and sequenced. The nucleotide sequence obtained
 CC (pyG) was used to design antisense PCR primers to amplify the
 CC 5' and 3' ends of the cDNA. These 5' and 3' clones are denoted p5V2 and
 CC p3V2 respectively. The entire base sequence for the 158 amino acid
 CC microheterogeneous B subunit and the 135 amino acid microheterogeneous B
 CC subunit are shown in AAQ28955 and AAQ28956. (Updated on 25-MAR-2003 to
 CC correct PN field.) (Updated on 25-MAR-2003 to correct PD field.)

XX Sequence 158 AA;

SQ Query Match 100.0%; Score 846; DB 2; Length 158;

```
Best Local Similarity 100.0%; Pred. No. 4e-86;
Matches 158; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

Qy 1 MIAAMKLFICFLQVLAGIHLVSGALSAGNNSTEMEVVYGRSVCGRPMKLVYTADE 60
Db 1 MIAAMKLFICFLQVLAGIHLVSGALSAGNNSTEMEVVYGRSVCGRPMKLVYTADE 60
Qy 61 HPNEVSHIFSPSCVLLSRSQGCGDGEGLHCVALKTANTMQILKIPPRDPHSYVENTFS 120
Db 61 HPNEVSHIFSPSCVLLSRSQGCGDGEGLHCVALKTANTMQILKIPPRDPHSYVENTFS 120
Qy 121 QDVLCERPILETTKAERRKTKGKRKQSKTPOTEPEHL 158
Db 121 QDVLCERPILETTKAERRKTKGKRKQSKTPOTEPEHL 158

RESULT 3

AAR22349

ID AAR22349 standard; protein; 158 AA.

XX AC AAR22349;

XX DT 29-JUL-1992 (first entry)

XX DE Rat VEGF-II 135 amino acid mauture B-subunit.

XX XX

DE Rat VEGF-II; mammalian glioma cell; conditioned medium; heterodimer;

KW KW homodimer; mitogenesis; vascular repair; blood vessel implant.

XX OS Rattus.

XX XX

Rattus.

XX XX

Key Location/Qualifiers

FH 1. .23

FT Peptide

FT 1/label= signal

FT 24. .158

FT Protein

FT 1/label= mature_VEGF_B_monomer

FT 24. .53

FT Peptide

FT 1/label= [I44]

FT /note= "Leu C cleavage peptide"

FT 30. .32

FT Modified-site

FT 1/label= N-glycosylation

FT 54. .94

FT Peptide

FT 1/label= [I44]

FT /label= Leu C cleavage peptide

FT 105. .104

FT Peptide

FT 1/label= L35

FT /note= "Leu C cleavage peptide"

FT 150. .158

FT Peptide

FT 1/label= L26

FT /note= "Leu C cleavage peptide"

XX XX

XX EP476983-A.

XX PD 25-MAR-1992.

CC	The novel growth factors are useful for the production or coverage of
CC	artificial blood vessels with vascular endothelial cell. They are also
CC	useful for the induction of tissue growth and repair
XX	
SQ	Sequence 158 AA;
Query Match	100.0% ; Score 846; DB 3 ; Length 158;
Best Local Similarity	100.0% ; Pred. No. 4e-86;
Matches	158; Conservative 0; Mismatches 0; Indels 0 ; Gaps
Qy	1 MIAAKLFTCFLQVLAGLVAVHSGQALSAGNNSTEMEVPPNEVGNSYCRPMKLYIADAE 6
Db	1 MIAAKLFTCFLQVLAGLVAVHSGQALSAGNNSTEMEVPPNEVGNSYCRPMKLYIADAE 6
Qy	61 HPMEVSHIFSPSPCVLLSRCSGCCGDEGLHCVALKTANITMQILKIPPNRDPHSYVEMTS 11
Db	61 HPMEVSHIFSPSPCVLLSRCSGCCGDEGLHCVALKTANITMQILKIPPNRDPHSYVEMTS 11
Qy	121 QDVLCBCECPILETTKAERRKTKGKRSKTPQESEPHL 158
Db	121 QDVLCBCECPILETTKAERRKTKGKRSKTPQESEPHL 158
RESULT 7	
ID	AAB37508 standard; protein; 158 AA.
XX	
AC	ABAB37508;
XX	
DT	26-FEB-2001 (first entry)
XX	
DE	Rat VEGF subunit B SEQ ID NO: 39.
XX	
KW	vascular endothelial growth factor; VEGF C subunit; cell division;
KW	artificial blood vessel; tissue growth; tissue repair.
OS	Rattus sp.
XX	
FN	US6140073-A.
XX	
PD	31-OCT-2000.
XX	
PF	96US-00586039.
XX	
PR	28-MAR-1991; 91US-00676436.
PR	20-SEP-1993; 93US-00124259.
XX	
PA	(MERCK) MERCK & CO INC.
XX	
PI	Thomas KA, Bayne ML;
XX	
DR	WPI: 2001-014858/02.
DR	N-PSDB; AAC33515.
XX	
PT	Human vascular endothelial cell growth factor (VEGF) C subunit DNA and
PT	protein, useful for promoting vascular development and repair, and for
PT	promoting tissue repair, especially for treating wounds in mammals.
XX	
PS	Example 10; Fig 8; 58pp; English.
XX	
CC	The present invention is concerned with the human vascular endothelial
CC	growth factor (VEGF) C subunit. VEGF is a vascular endothelial cell
CC	mitogen and can be used to promote vascular development and repair. The
CC	subunit may exist as a homodimer or a heterodimer with the VEGF A or B
CC	subunit. VEGF can be used in the treatment of wounds of mammals, to cover
CC	artificial blood vessels with vascular endothelial cells, in the
CC	production of artificial blood vessels and to induce tissue repair or
CC	growth
XX	
SQ	Sequence 158 AA;
Query Match	100.0% ; Score 846; DB 4 ; Length 158;
Best Local Similarity	100.0% ; Pred. No. 4e-86;

Matches	158;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
Qy	1	MLAMKLFTCFIQLLAGLAVHSQGALSAGNNSTEMEVYPFNEYWGRSYCRPEMKLVYTADE	60						
Db	1	MLAMKLFTCFIQLLAGLAVHSQGALSAGNNSTEMEVYPFNEYWGRSYCRPEMKLVYTADE	60						
Qy	61	HPNEVSHIFSPSCVLISRCGCGDEGLHCAVALKTANITMQLKIPRNDRPHSYVEMTF	120						
Db	61	HPNEVSHIFSPSCVLISRCGCGDEGLHCAVALKTANITMQLKIPRNDRPHSYVEMTF	120						
Qy	121	QDVLCERPILETTKAERRRTKGKRQSKTPQTEEPHL	158						
Db	121	QDVLCERPILETTKAERRRTKGKRQSKTPQTEEPHL	158						
RESULT 9									
	AAB73964	ID	AAB73964	standard;	protein;	158	AA.		
	XX	XX	XX						
	AC	AC	AC						
	XX	XX	XX						
	DT	23-NOV-2001	(first entry)						
	XX	XX	XX						
	DE	Rat VEGF II B subunit mature 135 amino acid form.							
	XX	XX	XX						
	KW	Rat; vascular endothelial growth factor II; VEGF-II; wound healing;							
	KW	vascular repair; neovascularisation; tissue repair; VEGF II B subunit;							
	KW	vulnerary; angiogenesis.							
	XX	XX	XX						
	OS	Rattus sp.							
	XX	XX	XX						
	FH								
	FT								
	Peptide	1-.23							
	/label=	Signal_peptide							
	Protein								
	FT								
	24.	.158							
	/label=	VEGF II B subunit							
	XX	XX	XX						
	US6180107-B1.	US6180107-B1.	US6180107-B1.						
	PN	PN	PN						
	XX	XX	XX						
	PD	30-JAN-2001.	30-JAN-2001.						
	XX	XX	XX						
	PF	10-MAR-1998;	98US-00038199.						
	XX	XX	XX						
	PR	21-SEP-1990;	90US-00586638.						
	PR	05-JAN-1993;	93US-00000834.						
	PR	31-AUG-1994;	94US-00299185.						
	XX	XX	XX						
	PA	(MERI) MERCK & CO INC.							
	XX	XX	XX						
	PI	Bayne ML, Conn GL, Thomas KA;							
	XX	XX	XX						
	DR	WPI; 2001-256064/26.							
	DR	N-PSDB; AAF81273.							
	XX	XX	XX						
	PS	Claim 1; Fig 6; 46pp; English.							
	XX	XX	XX						
	CC	The invention relates to a method for stimulating angiogenesis or wound							
	CC	healing through vascular repair, neovascularisation or both. The method							
	CC	comprises administering to a patient a pharmaceutically effective amount							
	CC	of mammalian vascular endothelial growth factor II (VEGF-II) comprising a							
	CC	heterodimer of subunits A and B, or a homodimer of B subunits. VEGF-II is							
	CC	useful for vascular development and repair, promotion of tissue repair,							
	CC	and the production of artificial vessels. The present sequence is VEGF I							
	CC	B subunit							
	XX	XX	XX						
	SQ	Sequence 158 AA;							
	Query Match	100.0%;	Score 846;	DB 4;	Length 158;				
	Best Local Similarity	100.0%;	Pred. No. 4e-86;	Indels	0;	Gaps	0;		
	Matches	158;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps
Qy	1	MLAMKLFTCFIQLVLAGLAVHSQGALSAGNNSTEMEVYPFNEYWGRSYCRPEMKLVYTADE	60						
Db	1	MLAMKLFTCFIQLVLAGLAVHSQGALSAGNNSTEMEVYPFNEYWGRSYCRPEMKLVYTADE	60						
Qy	1	MLAMKLFTCFIQLVLAGLAVHSQGALSAGNNSTEMEVYPFNEYWGRSYCRPEMKLVYTADE	60						
Db	1	MLAMKLFTCFIQLVLAGLAVHSQGALSAGNNSTEMEVYPFNEYWGRSYCRPEMKLVYTADE	60						

QY 61 HPNEVSHIFSPSCVYLRSRGCCCGDEGHCVALKANTTMQILKIPPNRDPHSYYEMTFS 120
 DO 61 HPNEVSHIFSPSCVYLRSRGCCCGDEGHCVALKANTTMQILKIPPNRDPHSYYEMTFS 120

QY 121 QDVLCERPILETTKAERRKTKGKRQSKTPQTEBPHL 158
 DB 121 QDVLCERPILETTKAERRKTKGKRQSKTPQTEBPHL 158

RESULT 10
 ABU62003 ID ABU62003 standard; protein; 158 AA.
 XX AC ABU62003;
 XX DT 19-AUG-2003 (first entry)
 XX DS Amino acid sequence for rat VEGF I A subunit cleavage product #2.
 XX KW Rat; vascular endothelial growth factor II; VEGF II; mitogenesis;
 KW mammalian; vascular endothelial cell growth; tissue repair;
 KW vascular development; vascular repair; blood vessel growth;
 KW neovascularisation; artificial blood vessel; polymeric vessel; pulmonary;
 KW A subunit.
 OS Rattus sp.
 XX FH Key
 FT Peptide 1..23
 FT Protein /label= Signal_peptide
 FT Protein /label= Mature_secreted_VEGF_I_A_subunit
 XX PN US2003045471-A1.
 XX PD 06-MAR-2003.
 XX PF 08-FEB-2002; 2002US-00071370.
 XX PR 21-SEP-1990; 90US-00586638.
 PR 05-JAN-1993; 93US-00000834.
 PR 31-AUG-1994; 94US-00299185.
 PR 10-MAR-1998; 98US-0003199.
 PR 07-JUN-1999; 99US-00326879.
 XX PA (MERCK & CO INC.
 XX PI Bayne ML, Conn GL, Thomas KA;
 XX DR WPI: 2003-371473/35.
 XX DR N-PSDB; ACA62371.
 XX PT New heterodimeric vascular endothelial growth factor II comprising A and B subunits encoded by different genes, useful for preparing a composition for promoting vascular or tissue repair or neovascularization.
 XX PS Example 9: Fig 41-4K; 50pp; English.

The present invention relates to the isolation of vascular endothelial growth factor II (VEGF II), and the polynucleotide sequences encoding it. VEGF II is a heterodimer comprising A and B subunits that are encoded by different genes. VEGF II stimulates mitogenesis of mammalian vascular endothelial cells. VEGF II is useful for promoting tissue repair and for stimulating the growth of vascular endothelial cells. VEGF II can also be used for stimulating the growth of vascular endothelial cells in a patient to promote vascular development and repair, or blood vessel growth (neovascularisation). VEGF II can further be used to produce artificial blood vessels by creating synthetic polymeric vessels with VEGF II and implanting into them into a patient. After the implantation endothelial cells migrate into and grow on the artificial surface. The present sequence represents rat VEGF I A subunit cleavage product #2 Sequence 158 AA;

CC CC Growth, factor II (VEGF II), and the polynucleotide sequences encoding it. CC CC VEGF II is a heterodimer comprising A and B subunits that are encoded by CC CC different genes. VEGF II stimulates mitogenesis of mammalian vascular CC CC endothelial cells. VEGF II is useful for promoting tissue repair and for CC CC stimulating the growth of vascular endothelial cells. VEGF II can also be CC CC used for stimulating the growth of vascular endothelial cells in a patient to promote vascular development and repair, or blood vessel growth (neovascularisation). VEGF II can further be used to produce artificial blood vessels by creating synthetic polymeric vessels with VEGF II and implanting into them into a patient. After the implantation endothelial cells migrate into and grow on the artificial surface. The present sequence represents rat VEGF I A subunit cleavage product #2 Sequence 158 AA;

Query Match Score 846; DB 6; Length 158;
 Best Local Similarity 100.0%; Pred. No. 4e-86;
 Matches 158; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLANKLFTCFLQVLAGLAHSQAGALSAGNNSTENMVEVPPNEVGRSSCRPMEKLYIYADE 60
 Db 1 MLANKLFTCFLQVLAGLAHSQAGALSAGNNSTENMVEVPPNEVGRSSCRPMEKLYIYADE 60

QY 61 HPNEVSHITSPSCVLLSRSGCCDDEGHCVALKANTTMQILKIPPNRDPHSYYEMTFS 120
 Db 61 HPNEVSHITSPSCVLLSRSGCCDDEGHCVALKANTTMQILKIPPNRDPHSYYEMTFS 120

QY 121 QDVLCERPILETTKAERRKTKGKRQSKTPQTEBPHL 158
 Db 121 QDVLCERPILETTKAERRKTKGKRQSKTPQTEBPHL 158

RESULT 11
 ABU62006 ID ABU62006 standard; protein; 158 AA.
 XX AC ABU62006;
 XX DT 19-AUG-2003 (first entry)
 XX DB Amino acid sequence for rat VEGF II B subunit.
 XX FH Rat; vascular endothelial growth factor II; VEGF II; mitogenesis;
 KW mammalian; vascular endothelial cell growth; tissue repair;
 KW vascular development; vascular repair; blood vessel growth;
 KW neovascularisation; artificial blood vessel; polymeric vessel; pulmonary;
 KW B subunit.
 XX OS Rattus sp.
 XX FH Key
 FT Peptide 1..23
 FT Protein /label= Signal_Peptide
 FT Protein /label= Mature_secreted_VEGF_II_B_subunit
 XX PN US2003045471-A1.
 XX PD 06-MAR-2003.
 XX PF 08-FEB-2002; 2002US-00071370.
 XX PR 21-SEP-1990; 90US-00586638.
 PR 05-JAN-1993; 93US-00000834.
 PR 31-AUG-1994; 94US-00299185.
 PR 10-MAR-1998; 98US-0003199.
 PR 07-JUN-1999; 99US-00326879.
 XX PA (MERCK & CO INC.
 XX PI Bayne ML, Conn GL, Thomas KA;
 XX DR WPI: 2003-371473/35.
 XX DR N-PSDB; ACA62374.

New heterodimeric vascular endothelial growth factor II comprising A and B subunits encoded by different genes, useful for preparing a composition for promoting vascular or tissue repair or neovascularization.

Claim 6; Fig 6; 50pp; English.

The present invention relates to the isolation of vascular endothelial growth factor II (VEGF II), and the polynucleotide sequences encoding it. VEGF II is a heterodimer comprising A and B subunits that are encoded by different genes. VEGF II stimulates mitogenesis of mammalian vascular endothelial cells. VEGF II is useful for promoting tissue repair and for stimulating the growth of vascular endothelial cells. VEGF II can also be used for stimulating the growth of vascular endothelial cells in a patient to promote vascular development and repair, or blood vessel growth (neovascularisation). VEGF II can further be used to produce artificial blood vessels by creating synthetic polymeric vessels with VEGF II and implanting into them into a patient. After the implantation endothelial cells migrate into and grow on the artificial surface. The present sequence represents rat VEGF I A subunit cleavage product #2 Sequence 158 AA;

used for stimulating the growth of vascular endothelial cells in a patient to promote vascular development and repair, or blood vessel growth (neovascularisation). VEGF II can further be used to produce artificial blood vessels by treating synthetic polymeric vessels with VEGF II and implanting them into a patient. After the implantation the endothelial cells migrate into and grow on the artificial surface. The present sequence represents rat VEGF II B subunit.

Sequence 158 AA;

```
Query Match 100.0%; Score 846; DB 6; Length 158;
Best Local Similarity 100.0%; Prod. No. 4e-86;
Matches 158; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
SQ Sequence 158 AA;
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QY 1 MLANKLFTCFLQVLAGLAHSQGALSAGNINSTEVMVPPNEVGRSYCRPMELKLVIADE 60
Db 1 MLANKLFTCFLQVLAGLAHSQGALSAGNINSTEVMVPPNEVGRSYCRPMELKLVIADE 60
QY 61 HPNEVSHIFSPSCVILSRSGCCGDEGLHCVALKTANTTMQLIKIPRNDRPHSYVEMTFS 120
Db 61 HPNEVSHIFSPSCVILSRSGCCGDEGLHCVALKTANTTMQLIKIPRNDRPHSYVEMTFS 120
QY 121 QDVLCERPLLETTKAERKTKGKRQSKTPQTTEBPHL 158
Db 121 QDVLCERPLLETTKAERKTKGKRQSKTPQTTEBPHL 158
QY 121 QDVLCERPLLETTKAERKTKGKRQSKTPQTTEBPHL 158
Db 121 QDVLCERPLLETTKAERKTKGKRQSKTPQTTEBPHL 158
```

RESULT 13

```
ID AAR27356 standard; protein; 138 AA.
XX AC AAR27356;
```

```
XX DT 25-MAR-2003 (revised)
XX DT 25-FEB-1993 (first entry)
AC Sequence of vascular endothelial cell growth factor VEGF B 138 amino acid
DE residue subunit.
XX KW Vascular development; mitogen; blood vessel;
XX KW vascular endothelial growth factor; neovascularisation.
XX OS Rattus .
XX PF 27-MAR-1992; 92EP-00302750.
XX PR 28-MAR-1991; 91US-00676436.
XX PA (MERI ) MERCK & CO INC.
XX PI Bayne ML, Thomas KA;
XX DR WPI; 1992-325745/40.
XX DR N-PSDB; AAQ28955.
```

```
XX PT Vascular endothelial cell growth factor sub-units - which stimulate
vascular endothelial cell growth, used for inducing tissue repair and
growth.
XX Disclosure; Fig 7; 61pp; English.
XX CC The full length coding region of the B subunit or monomer of VEGF is
determined from four sets of overlapping cDNA clones. Degenerate oligo-
CC primers based on the amino acid sequences of polypeptides L50 are used
CC to PCR amplify the central region of the cDNA for VEGF AB monomer. A
CC single band migrating at 108 bp was gel purified, digested with Sall,
CC ligated into pEM321(+), and sequenced. The nucleotide sequence obtained
CC (pYG) was used to design antisense and sense PCR primers to amplify the
CC 5' and 3' ends of the cDNA. These 5', and 3' clones are denoted p5v2 and
CC p3v2 respectively. The entire base sequence for the 158 amino acid
CC microheterogeneous B subunit and the 138 amino acid microheterogeneous B
CC subunit are shown in AAQ28955 and AAQ28956. (Updated on 25-MAR-2003 to
CC correct PN field.) (Updated on 25-MAR-2003 to correct PD field.)
```

CC method and VEGF (a mitogen) are useful in inducing vascular or tissue
CC development and repair. The present sequence represents a rat VEGF
CC subunit.

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XX Query Match 100.0%; Score 846; DB 6; Length 158;
Best Local Similarity 100.0%; Prod. No. 4e-86;
Matches 158; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
SQ Sequence 158 AA;
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```
QY 1 MLANKLFTCFLQVLAGLAHSQGALSAGNINSTEVMVPPNEVGRSYCRPMELKLVIADE 60
Db 1 MLANKLFTCFLQVLAGLAHSQGALSAGNINSTEVMVPPNEVGRSYCRPMELKLVIADE 60
QY 61 HPNEVSHIFSPSCVILSRSGCCGDEGLHCVALKTANTTMQLIKIPRNDRPHSYVEMTFS 120
Db 61 HPNEVSHIFSPSCVILSRSGCCGDEGLHCVALKTANTTMQLIKIPRNDRPHSYVEMTFS 120
QY 121 QDVLCERPLLETTKAERKTKGKRQSKTPQTTEBPHL 158
Db 121 QDVLCERPLLETTKAERKTKGKRQSKTPQTTEBPHL 158
```

RESULT 13

```
ID AAR27356 standard; protein; 138 AA.
XX AC AAR27356;
```

```
XX DT 25-MAR-2003 (revised)
XX DT 25-FEB-1993 (first entry)
AC Sequence of vascular endothelial cell growth factor VEGF B 138 amino acid
DE residue subunit.
XX KW Vascular development; mitogen; blood vessel;
XX KW vascular endothelial growth factor; neovascularisation.
XX OS Rattus .
XX PF 27-MAR-1992; 92EP-00302750.
XX PR 28-MAR-1991; 91US-00676436.
XX PA (MERI ) MERCK & CO INC.
XX PI Bayne ML, Thomas KA;
XX DR WPI; 1992-325745/40.
XX DR N-PSDB; AAQ28955.
```

```
XX PT Vascular endothelial cell growth factor sub-units - which stimulate
vascular endothelial cell growth, used for inducing tissue repair and
growth.
XX Disclosure; Fig 7; 61pp; English.
XX CC The full length coding region of the B subunit or monomer of VEGF is
determined from four sets of overlapping cDNA clones. Degenerate oligo-
CC primers based on the amino acid sequences of polypeptides L50 are used
CC to PCR amplify the central region of the cDNA for VEGF AB monomer. A
CC single band migrating at 108 bp was gel purified, digested with Sall,
CC ligated into pEM321(+), and sequenced. The nucleotide sequence obtained
CC (pYG) was used to design antisense and sense PCR primers to amplify the
CC 5' and 3' ends of the cDNA. These 5', and 3' clones are denoted p5v2 and
CC p3v2 respectively. The entire base sequence for the 158 amino acid
CC microheterogeneous B subunit and the 138 amino acid microheterogeneous B
CC subunit are shown in AAQ28955 and AAQ28956. (Updated on 25-MAR-2003 to
CC correct PN field.) (Updated on 25-MAR-2003 to correct PD field.)
```

CC chromatography and reverse phase chromatography. See also AAQ23038,
 SQ Sequence 138 AA;
 XX CC AAQ23040 and AAQ23042-Q23059
 XX SQ Sequence 138 AA;

Query Match 87.5%; Score 740; DB 2; Length 138;
 Best Local Similarity 100.0%; Pred. No. 2.3e-74;
 Matches 138; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX Query Match 87.5%; Score 740; DB 2; Length 138;
 Best Local Similarity 100.0%; Pred. No. 2.3e-74;
 Matches 138; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLANKLFTCFLQVLAGLAHSQGALSAGNNSTEMEVPPNEVGRSYCRPMEKLYIADE 60
 Db 1 MLANKLFTCFLQVLAGLAHSQGALSAGNNSTEMEVPPNEVGRSYCRPMEKLYIADE 60
 QY 61 HPNEVSHIISPSCVLILRSQCGCCDGEGLHCVALKTANTTMQILKIPPNRDPHSTVEMTFS 120
 Db 61 HPNEVSHIISPSCVLILRSQCGCCDGEGLHCVALKTANTTMQILKIPPNRDPHSTVEMTFS 120
 QY 121 QDVLCERCPPILETTKAER 138
 Db 121 QDVLCERCPPILETTKAER 138
 QY 121 QDVLCERCPPILETTKAER 138
 Db 121 QDVLCERCPPILETTKAER 138

RESULT 15
 AAR22350 standard; protein; 138 AA.
 XX ID AAWS3645 standard; protein; 138 AA.
 AC XX
 AC XX
 AC AAWS3645;
 DT 30-JUL-1998 (first entry)
 DE VEGF-II 115 amino acid mature B-subunit.
 XX KW mammalian Glioma cell; conditioned medium; heterodimer;
 KW homodimer; mitogenesis; vascular repair; blood vessel implant.
 XX Rattus.
 OS Rattus sp.
 FH XX
 FT 1.23
 FT 1.23 (first entry)
 FR 24..138 (first entry)
 Protein /label= mature_VEGF_B_monomer
 FT Modified-site 30..32
 FT /label= N-glycosylation
 FT Modified-site 97..99
 FT /label= N-glycosylation
 XX EP47693-A.
 PN XX
 PD 25-MAR-1992.
 XX PI Conn GL, Thomas KA, Bayne ML;
 PP 18-SEP-1991; 91EP-00308489.
 PR 21-SEP-1990; 90US-00586638.
 PR 21-SEP-1990; 90US-00586640.
 PA (MERI) MERCK & CO INC.
 XX PT
 PI Conn GL, Thomas KA, Bayne ML;
 PR 21-SEP-1990; 90US-00586638.
 DR 05-JAN-1993; 93US-00000834.
 XX PT
 PR 21-SEP-1990; 90US-00586638.
 DR 05-JAN-1993; 93US-00000834.

Example 9; Fig 4; 46pp; English.

XX The present sequence represents a rat vascular endothelial growth factor
 CC I (VEGF I) A subunit. The present invention describes: (1) a mammalian
 CC VEGF II protein comprising an A subunit from AAWS3639, AAWS3640 or
 CC AAWS3641, and a B subunit from AAWS3638, AAWS53639 or the first 115-135
 CC amino acids of AAWS3638; and (2) a mammalian VEGF comprising a
 CC heterodimer or homodimer of B subunits. The growth factor is used for
 CC promoting vascular development and repair and for promoting tissue repair
 XX SQ Sequence 138 AA;

Query Match 87.5%; Score 740; DB 2; Length 138;
 Best Local Similarity 100.0%; Pred. No. 2.3e-74;
 Matches 138; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLANKLFTCFLQVLAGLAHSQGALSAGNNSTEMEVPPNEVGRSYCRPMEKLYIADE 60

Db	1	MLAMKLFTCFLQVLAGLAHSQGALSAGNNSTENEVPPNEVNGRSYCRPMEKLVIADE	60
Qy	61	HPNEVSHITSPSCVLLSRCGCCDDEGHCVALKTANTTMQILKIPPNRDPHSYVEMTFS	120
Db	61	HPNEVSHITSPSCVLLSRCGCCDDEGHCVALKTANTTMQILKIPPNRDPHSYVEMTFS	120
Qy	121	QDVLCRPLLETKAER	138
Db	121	QDVLCRPLLETKAER	138

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Job time : 131 secs

W. C. A. N.
Westgate

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OM protein - protein search, using sw model

Run on: September 13, 2004, 09:48:49 ; Search time 32 Seconds
(without alignments)
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Perfect score: 846

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Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters:

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the total score distribution, and is derived by analysis of the total score distribution.

SUMMARIES

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1	846	100.0	158	3	US-08-586-039B-39	Sequence 39, Appl
2	846	100.0	158	4	US-08-586-039B-39	Sequence 39, Appl
3	740	87.5	138	3	US-08-586-039B-37	Sequence 37, Appl
4	740	87.5	138	4	US-08-586-039B-37	Sequence 37, Appl
5	501.5	59.3	170	2	US-08-039-297B-8	Sequence 8, Appl
6	501.5	59.3	170	3	US-08-586-039B-45	Sequence 45, Appl
7	501.5	59.3	170	4	US-08-586-039B-45	Sequence 45, Appl
8	499.5	59.0	170	4	US-08-431-888-5	Sequence 5, Appl
9	498.5	58.9	154	4	US-08-586-039B-41	Sequence 41, Appl
10	498.5	58.9	154	4	US-08-586-039B-41	Sequence 41, Appl
11	474.5	56.1	149	1	US-08-469-427A-14	Sequence 14, Appl
12	474.5	56.1	149	2	US-08-469-427A-14	Sequence 2, Appl
13	474.5	56.1	149	2	US-08-569-063C-21	Sequence 21, Appl
14	474.5	56.1	149	3	US-08-795-030-55	Sequence 55, Appl
15	474.5	56.1	149	3	US-08-586-039B-47	Sequence 47, Appl
16	474.5	56.1	149	4	US-09-355-700-55	Sequence 55, Appl
17	474.5	56.1	149	4	US-08-106-054A-5	Sequence 5, Appl
18	474.5	56.1	149	4	US-09-699-169-47	Sequence 47, Appl
19	474.5	56.1	149	4	US-09-313-299-5	Sequence 5, Appl
20	474.5	56.1	149	4	US-08-671-573B-54	Sequence 54, Appl
21	319.5	37.8	214	3	US-08-586-039B-35	Sequence 35, Appl
22	319.5	37.8	214	4	US-09-699-169-35	Sequence 35, Appl
23	316	37.4	214	6	5240848-11	Patent No. 5240848
24	315	37.2	188	4	US-09-244-583-28	Sequence 28, Appl
25	315	37.2	213	4	US-09-574-708A-8	Sequence 8, Appl
26	315	37.2	213	3	US-08-586-039B-49	Sequence 49, Appl
27	315	37.2	215	4	US-09-699-169-49	Sequence 49, Appl

ALIGNMENTS

28	315	37.2	215	4	US-09-392-931-8	Sequence 8, Appl
29	315	37.2	232	2	US-08-999-811-7	Sequence 7, Appl
30	315	37.2	232	3	US-08-824-996-9	Sequence 9, Appl
31	315	37.2	232	4	US-09-042-155-7	Sequence 7, Appl
32	315	37.2	232	4	US-09-574-708A-10	Sequence 10, Appl
33	315	37.2	232	4	US-08-465-968-5	Sequence 5, Appl
34	315	37.2	231	5	PCT-US96-09001-10	Sequence 10, Appl
35	314.5	37.2	231	5	US-09-037-983C-16	Sequence 16, Appl
36	313.5	37.1	138	4	US-08-807-992B-3	Sequence 3, Appl
37	313.5	37.1	215	3	US-08-907-992B-3	Sequence 4, Appl
38	313.5	37.1	232	3	US-08-907-992B-4	Sequence 17, Appl
39	312.5	36.9	137	4	US-09-037-983C-17	Sequence 2, Appl
40	312.5	36.9	145	4	US-09-392-932-2	Sequence 2, Appl
41	312.5	36.9	145	4	US-09-574-708A-4	Sequence 4, Appl
42	312.5	36.9	145	4	US-09-428-909A-2	Sequence 2, Appl
43	312.5	36.9	145	4	US-09-392-931-4	Sequence 4, Appl

QY 1 MLAMKLFICFLQVLAGLAHSQAGLSAGNNSTEMEVNGRSYCRPMEMKLVIADE 60
 Db 1 MLAMKLFICFLQVLAGLAHSQAGLSAGNNSTEMEVNGRSYCRPMEMKLVIADE 60
 QY 61 HPNEVSHIFSPSCVILSRSGCCGDEGLHCVALKTANTMQILKIPPNRDPHSYVENTFS 120
 Db 61 HPNEVSHIFSPSCVILSRSGCCGDEGLHCVALKTANTMQILKIPPNRDPHSYVENTFS 120
 QY 121 QDVLCBCECRPILETTKAERRKTKGRKQSKTPQTEEPHL 158
 Db 121 QDVLCBCECRPILETTKAERRKTKGRKQSKTPQTEEPHL 158

RESULT 2

US-09-699-769-39

Sequence 39 Application US/09699769

Patent No. 6569434

GENERAL INFORMATION:

APPLICANT: Bayne, Marvin L.

Thomas Jr., Kenneth A.

TITLE OF INVENTION: VASCULAR ENDOTHELIAL CELL GROWTH FACTOR

C SUBUNIT

NUMBER OF SEQUENCES: 49

GENERAL INFORMATION ADDRESS:

ADDRESSEE: Merck & Co., Inc.

STREET: 126 E. Lincoln Avenue

CITY: Railway

STATE: New Jersey

COUNTRY: USA

ZIP: 07065-0900

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Microsoft Word 6

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/699,769

FILING DATE: 30-Oct-2000

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/586,039

FILING DATE: 16-JAN-1996

APPLICATION NUMBER: 08/124,259

FILING DATE: 20-SEP-1993

APPLICATION NUMBER: 07/676,436

FILING DATE: 28-MAR-1991

ATTORNEY/AGENT INFORMATION:

NAME: Hand, J. Mark

REGISTRATION NUMBER: 36,545

REFERENCE/DOCKET NUMBER: 18361DB

TELECOMMUNICATION INFORMATION:

TELEPHONE: (732) 594-3905

TELEFAX: (732) 594-4720

INFORMATION FOR SEQ ID NO: 39:

SEQUENCE CHARACTERISTICS:

LENGTH: 158 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLogy: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 39:

US-09-699-769-39

Query Match Score 100.0%; Score 846; DB 4; Length 158;
 Best Local Similarity 100.0%; Pred. No. 6.5e-31; Indels 0; Gaps 0;
 Matches 158; Conservative 0; Mismatches 0; Gaps 0;

1 MLAMKLFICFLQVLAGLAHSQAGLSAGNNSTEMEVNGRSYCRPMEMKLVIADE 60
 1 MLAMKLFICFLQVLAGLAHSQAGLSAGNNSTEMEVNGRSYCRPMEMKLVIADE 60

RESULT 4

Db 61 HPNEVSHIFSPSCVILSRSGCCGDEGLHCVALKTANTMQILKIPPNRDPHSYVENTFS 120
 QY 121 QDVLCBCECRPILETTKAERRKTKGRKQSKTPQTEEPHL 158
 Db 121 QDVLCBCECRPILETTKAERRKTKGRKQSKTPQTEEPHL 158

RESULT 3

US-08-586-039B-37

Sequence 37 Application US/0886039B

Patent No. 6140073

GENERAL INFORMATION:

APPLICANT: Bayne, Marvin L.

GENERAL INFORMATION ADDRESS:

ADDRESSEE: Merck & Co., Inc.

STREET: 126 E. Lincoln Avenue

CITY: Railway

STATE: New Jersey

COUNTRY: USA

ZIP: 07065-0900

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Microsoft Word 6

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/586,039B

FILING DATE: 16-JAN-1996

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/124,259

FILING DATE: 20-SEP-1993

REFERENCE/DOCKET NUMBER: 18361DA

TELECOMMUNICATION INFORMATION:

TELEPHONE: (908) 594-3905

TELEFAX: (908) 594-4720

INFORMATION FOR SEQ ID NO: 37:

SEQUENCE CHARACTERISTICS:

LENGTH: 138 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLogy: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 39:

US-08-586-039B-37

Query Match Score 87.5%; Score 740; DB 3; Length 138;

Best Local Similarity 100.0%; Pred. No. 1.3e-18; Indels 0; Gaps 0;

Matches 138; Conservative 0; Mismatches 0;

1 MLAMKLFICFLQVLAGLAHSQAGLSAGNNSTEMEVNGRSYCRPMEMKLVIADE 60
 1 MLAMKLFICFLQVLAGLAHSQAGLSAGNNSTEMEVNGRSYCRPMEMKLVIADE 60

61 HPNEVSHIFSPSCVILSRSGCCGDEGLHCVALKTANTMQILKIPPNRDPHSYVENTFS 120
 61 HPNEVSHIFSPSCVILSRSGCCGDEGLHCVALKTANTMQILKIPPNRDPHSYVENTFS 120

121 QDVLCBCECRPILETTKAER 138
 121 QDVLCBCECRPILETTKAER 138

TITLE OF INVENTION: NUCLEOTIDE SEQUENCES CODING FOR A PROTEIN WITH ANGIOGENESIS REGULATIVE PROPERTIES
 Sequence 37, Application US/09699769
 Patent No. 656434
 GENERAL INFORMATION:
 APPLICANT: Bayne, Marvin L.
 Thomas Jr., Kenneth A.
 TITLE OF INVENTION: VASCULAR ENDOTHELIAL CELL GROWTH FACTOR
 NUMBER OF SEQUENCES: 49
 CORRESPONDENCE ADDRESS:
 ADDRESS: Merck & Co., Inc.
 STREET: 126 E. Lincoln Avenue
 CITY: Rahway
 STATE: New Jersey
 COUNTRY: USA
 ZIP: 07065-0900
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Microsoft Word 6
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/699,769
 FILING DATE: 20-OCT-2000
 CLASSIFICATION: <Unknown>
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 08/586,039
 FILING DATE: 16-JAN-1996
 APPLICATION NUMBER: 08/124,259
 FILING DATE: 27-SEP-1993
 APPLICATION NUMBER: 08/124,436
 FILING DATE: 28-MAR-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Hand, J. Mark
 REGISTRATION NUMBER: 36,545
 REFERENCE/DOCKET NUMBER: 18361DB
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (732) 594-3905
 TELEFAX: (732) 594-4720
 INFORMATION FOR SEQ ID NO: 37:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 138 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 37:
 US 09-699-769-37

Query Match 59.3%; Score 501.5; DB 2; Length 170;
 Best Local Similarity 61.5%; Pred No. 1.2e-50; Indels 5; Gaps 2;
 Matches 96; Conservative 23; Mismatches 32; Indels 5; Gaps 2;

QY 1 M L A M K L F T C F L Q V I A G L A V H S - - - Q G A L S A G N N S T E M V V P P N E V W G R S Y C R P M E K L V Y 56
 Db 1 M P V N R L F P C F L Q V I A G L A V H S - - - Q G A L S A G N N S T E M V V P P N E V W G R S Y C R P M E K L V Y 56

QY 57 I A D B P N E V H I T S P C V I L L S R G C C D E G L R C V A L K T A N I T M Q I L K I P P N R D P H S Y T E 116
 Db 61 V V S E P V S E Y H M F S P C V I L L S R G C C D E G L R C V A L K T A N I T M Q I L K I P P N R D P H S Y T E 116

QY 117 M T F S Q D V I L C E C R P I L E T T A E R R K T K G K R K Q S K T P Q 152
 Db 120 L T F S Q H V R C E C R P I L E T T A E R R K T K G K R K Q S K T P Q 155

RESULT 6 US-08-586-039B-45
 US-08-586-039B-45
 ; Sequence 45, Application US/08586039B
 ; Patent No. 6140013

GENERAL INFORMATION:
 APPLICANT: Bayne, Marvin L.
 Thomas Jr., Kenneth A.
 TITLE OF INVENTION: VASCULAR ENDOTHELIAL CELL GROWTH FACTOR C
 NUMBER OF SEQUENCES: 49
 CORRESPONDENCE ADDRESS:
 ADDRESS: Merck & Co., Inc.
 STREET: 126 E. Lincoln Avenue
 CITY: Rahway
 STATE: New Jersey
 COUNTRY: USA

RESULT 5 US-08-039-297B-8
 US-08-039-297B-8
 ; Sequence 8, Application US/08039297B
 ; Patent No. 5919839

GENERAL INFORMATION:
 APPLICANT: Perico, Maria
 Magione, Domenico
 APPLICANT: Magione, Domenico
 APPLICANT: Perico, Maria

ZIP: 07065-0900
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Microsoft Word 6
 CURRENT APPLICATION NUMBER:
 APPLICATION NUMBER: US/08/586,039B
 FILING DATE: 16-JAN-1996
 CLASSIFICATION:
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 08/124,259
 FILING DATE: 20-SEP-1993
 APPLICATION NUMBER: 07/676,436
 FILING DATE: 28-MAR-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Hand, J. Mark
 REGISTRATION NUMBER: 36,545
 REFERENCE/DOCKET NUMBER: 18361DA
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (908) 594-3905
 TELEFAX: (908) 594-4720
 INQUIRIES: (908) 594-4720
 SEQUENCE CHARACTERISTICS:
 LENGTH: 170 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 INQUIRIES FOR SEQ ID NO: 45:
 LENGTH: 170 amino acids
 SEQUENCE CHARACTERISTICS:
 LENGTH: 170 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-586-039B-45

Query Match 59.3%; Score 501.5; DB 3; Length 170;
 Best Local Similarity 61.5%; Prod. No. 1.2e-50; Indels 5; Gaps 2;
 Matches 96; Conservative 23; Mismatches 32; Indels 5; Gaps 2;

Qy 1 MIAAMKLFICFLQVLAGLAVHS---QGALSAGNINSTEVVPPNEVGWSYCRPMELVY 56
 Db 1 MPYMRLLFFCFLQVLAGLALPAVPPQQWALSAGNSSEEVVPQEVWGRSYCRALEIYD 60

Query Match 59.3%; Score 501.5; DB 3; Length 170;
 Best Local Similarity 61.5%; Prod. No. 1.2e-50; Indels 5; Gaps 2;
 Matches 96; Conservative 23; Mismatches 32; Indels 5; Gaps 2;

Qy 57 IADEHPEVSHIFSPSCVLLRSQSGCCDEGLHCVALKTANTTMQLIKIPPNRDPHSEYV 116
 Db 61 VVSEYPSEVEHMSPSCVSLRGTGCCDENLHCVPVBTANVTMQLIKIRSQRDP-SYVE 119

Query Match 59.3%; Score 501.5; DB 3; Length 170;
 Best Local Similarity 61.5%; Prod. No. 1.2e-50; Indels 5; Gaps 2;
 Matches 96; Conservative 23; Mismatches 32; Indels 5; Gaps 2;

Qy 117 MTPSQDVLCERPILETTKAERRKTKGKRQSKTPQ 152
 Db 120 LTPSQRTCECRPILETTKAERRKTKGKRQSKTPQ 155

RESULT 8
 US-09-699-769-45
 ; Sequence 5, Application US/02431888A
 ; Patent No. 6541008
 ; GENERAL INFORMATION:
 ; APPLICANT: Wise, Lyn M
 ; APPLICANT: Mercer, Andrew A
 ; APPLICANT: Savory, Loreen J
 ; APPLICANT: Slacker, Stephen B
 ; TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR-LIKE PROTEIN FROM ORF
 ; TITLE OF INVENTION: VIRUS N22 BINDS AND ACTIVATES MAMMALIAN VEGF
 ; FILE REFERENCE: Sequence Listing for 09/431,833
 ; Patent No. 6541008
 ; CURRENT APPLICATION NUMBER: US/09/431,888A
 ; CURRENT FILING DATE: 1999-11-02
 ; EARLIER APPLICATION NUMBER: 60/106,689
 ; EARLIER FILING DATE: 1998-11-02
 ; EARLIER APPLICATION NUMBER: 60/106,800
 ; EARLIER FILING DATE: 1998-11-03
 ; NUMBER OF SEQ ID NOS: 11
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 5
 ; LENGTH: 170
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens

ZIP: 07065-0900
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Microsoft Word 6
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/699,769
 FILING DATE: 30-Oct-2000

CLASSIFICATION: <Unknown>
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 08/586,039
 FILING DATE: 16-JAN-1996
 APPLICATION NUMBER: 08/124,259
 FILING DATE: 20-SEP-1993
 APPLICATION NUMBER: 07/676,436
 FILING DATE: 28-MAR-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Hand, J. Mark
 REGISTRATION NUMBER: 36,545
 REFERENCE/DOCKET NUMBER: 18361DB
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (732) 594-3905
 TELEFAX: (732) 594-4720
 INFORMATION FOR SEQ ID NO: 45:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 170 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 45:
 US-09-699-769-45

Query Match 59.3%; Score 501.5; DB 4; Length 170;
 Best Local Similarity 61.5%; Prod. No. 1.2e-50; Indels 5; Gaps 2;
 Matches 96; Conservative 23; Mismatches 32; Indels 5; Gaps 2;

Qy 1 MIAAMKLFICFLQVLAGLAVHS---QGALSAGNINSTEVVPPNEVGWSYCRPMELVY 56
 Db 1 MPYMRLLFFCFLQVLAGLALPAVPPQQWALSAGNSSEEVVPQEVWGRSYCRALEIYD 60

Query Match 59.3%; Score 501.5; DB 4; Length 170;
 Best Local Similarity 61.5%; Prod. No. 1.2e-50; Indels 5; Gaps 2;
 Matches 96; Conservative 23; Mismatches 32; Indels 5; Gaps 2;

Qy 57 IADEHPEVSHIFSPSCVLLRSQSGCCDEGLHCVALKTANTTMQLIKIPPNRDPHSEYV 116
 Db 61 VVSEYPSEVEHMSPSCVSLRGTGCCDENLHCVPVBTANVTMQLIKIRSQRDP-SYVE 119

Query Match 59.3%; Score 501.5; DB 4; Length 170;
 Best Local Similarity 61.5%; Prod. No. 1.2e-50; Indels 5; Gaps 2;
 Matches 96; Conservative 23; Mismatches 32; Indels 5; Gaps 2;

Qy 117 MTPSQDVLCERPILETTKAERRKTKGKRQSKTPQ 152
 Db 120 LTPSQRTCECRPILETTKAERRKTKGKRQSKTPQ 155

RESULT 8
 US-09-699-769-45
 ; Sequence 5, Application US/02431888A
 ; Patent No. 6541008
 ; GENERAL INFORMATION:
 ; APPLICANT: Wise, Lyn M
 ; APPLICANT: Mercer, Andrew A
 ; APPLICANT: Savory, Loreen J
 ; APPLICANT: Slacker, Stephen B
 ; TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR
 ; TITLE OF INVENTION: VEGF
 ; FILE REFERENCE: Sequence Listing for 09/431,833
 ; Patent No. 6541008
 ; CURRENT APPLICATION NUMBER: US/09/431,888A
 ; CURRENT FILING DATE: 1999-11-02
 ; EARLIER APPLICATION NUMBER: 60/106,689
 ; EARLIER FILING DATE: 1998-11-02
 ; EARLIER APPLICATION NUMBER: 60/106,800
 ; EARLIER FILING DATE: 1998-11-03
 ; NUMBER OF SEQ ID NOS: 11
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 5
 ; LENGTH: 170
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens

Query Match 59.0%; DB 4; Length 170;
 Best Local Similarity 61.5%; Prod. No. 2e-50;

RESULT 11
US-08-427A-14 Application US/08469427A
Sequence 14; Patent No. 5,679,8

GENERAL INFORMATION:
APPLICANT: Eriksson, Ulf
APPLICANT: Olofsson, Birgitta
APPLICANT: Alitalo, Kari
APPLICANT: Pajusola, Katri
TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR-B AND
TITLE OF INVENTION: DNA CODING THEREFOR

NUMBER OF SEQUENCES: 17
ADDRESSEE: Evanson, McKeown, Edwards & Lenahan
STREET: 1200 G Street, N.W., Suite 700
CITY: Washington
STATE: DC
ZIP: 20005

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,427A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/397,651
FILING DATE: 01-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Evans, Joseph D
REGISTRATION NUMBER: 26,269
REFERENCE DOCKET NUMBER: 41979cp2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-8800
TELEFAX: (202) 628-8844
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 149 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Protein
US-08-469-427A-14

Query Match Score 474.5; DB 1; Length 149;
Best Local Similarity 64.1%; Pred. No. 1.4e-47;
Matches 91; Conservative 19; Mismatches 27; Indels 5; Gaps 2;

Qy 1 MLAMKLFICFLQVLAGLAVHS----OGLASAGNNSTMEEVPPNEVGRSYCRPMELVY 56
Db 1 MPYMRLLFCFLQVLAGLPAVPPQQWALSAGNSSEVEVPPQEVNGRSYCRALERLVD 60

Query Match Score 474.5; DB 1; Length 149;
Best Local Similarity 64.1%; Pred. No. 1.4e-47;
Matches 91; Conservative 19; Mismatches 27; Indels 5; Gaps 2;

Qy 1 TAEDHPNVEVSHSPSCVLLSREGGCCDEGLHVALKNTANTMQLIKIPPNRDPHRYVE 116
Db 1 VVSEYPSEVHEMSPSCVLLRTGCCDENLHCVPVETANTMQLIKRGDRP-SYVE 119

RESULT 12
US-08-039-297B-2 Application US/08039297B
Sequence 2; Patent No. 5,919,899
GENERAL INFORMATION:
APPLICANT: PERISCO, MARIA
APPLICANT: MAGIONE, DOMENICO
TITLE OF INVENTION: NUCLEOTIDE SEQUENCES CODING FOR A
TITLE OF INVENTION: HUMAN
TITLE OF INVENTION: PROTEIN WITH ANGIOGENESIS REGULATIVE PROPERTIES

NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: BEVERIDGE, DEGRANDI, WEILACHER & YOUNG,
STREET: 1850 M Street, N.W.
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/039,297B
FILING DATE: 19-APR-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IT 48315-A90\
FILING DATE: 27-SEP-1990
ATTORNEY/AGENT INFORMATION:
NAME: Weilacher, Robert G
REGISTRATION NUMBER: 20,531
REFERENCE DOCKET NUMBER: 48573
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-659-2811
TELEFAX: 202-659-1462
TELEX: WU164470
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 149 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
US-08-039-297B-2

Query Match Score 474.5; DB 2;
Best Local Similarity 64.1%; Pred. No. 1.4e-47;
Matches 91; Conservative 19; Mismatches 27; Indels 5; Gaps 2;

Qy 1 MLAMKLFICFLQVLAGLAVHS---OGLASAGNNSTMEEVPPNEVGRSYCRPMELVY 56
Db 1 MPYMRLLFCFLQVLAGLPAVPPQQWALSAGNSSEVEVPPQEVNGRSYCRALERLVD 60

Query Match Score 474.5; DB 1; Length 149;
Best Local Similarity 64.1%; Pred. No. 1.4e-47;
Matches 91; Conservative 19; Mismatches 27; Indels 5; Gaps 2;

Qy 57 IADEPHNVEVSHSPSCVLLSREGGCCDEGLHVALKNTANTMQLIKIPPNRDPHRYVE 116
Db 61 VVSEYPSEVHEMSPSCVLLRTGCCDENLHCVPVETANTMQLIKRGDRP-SYVE 119

RESULT 13
US-08-569-063C-21 Application US/08569063C
Sequence 21; Patent No. 5,928939
GENERAL INFORMATION:
APPLICANT: ERIKSSON, Ulf
APPLICANT: OLOFSSON, Birgitta
APPLICANT: ALITALO, Kari
APPLICANT: PAJUSOLA, Katri
TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR-B AND
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Evenson, McKeown, Edwards & Lenahan, P.L.L.C.
STREET: 1200 G Street, N.W., Suite 700
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/569,063C
 FILING DATE: 06-DEC-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/469,427
 FILING DATE: 06-JUN-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/397,651
 FILING DATE: 01-MAR-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: EVANS, Joseph D
 REGISTRATION NUMBER: 26,269
 REFERENCE/DOCKET NUMBER: 1064/41979CP3
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 628-8800
 TELEFAX: (202) 628-8844
 INFORMATION FOR SEQ ID NO: 21:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 149 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-569-063C-21

Query Match Score 474.5; DB 2; Length 149;
 Best Local Similarity 64.1%; Pred. No. 1.4e-47;
 Matches 91; Conservative 19; Mismatches 27; Indels 5; Gaps 2;

Qy 1 MLMKLFFPLQLAGLAVHS---QGALISAGNSTMENVVPNEWGRSICRPMELVY 56
 Db 1 MPYWRLLFPFLQLAGLAVPAVPPQQWALASAGNSSEEVVVFQEVMGRSYCRALERLVD 60

Qy 57 IADEHPNEYSHIFSPSCVLLSRCSGCCGDBGLHCVALKTANITMQLIKPPNNDPHSYVE 116
 Db 61 VVSEYPSEVEHMFSPSCVLLSRCSGCCGDBGLHCVALKTANITMQLIKPPNNDPHSYVE 119

Qy 117 MTFSODVLCCEPRLTEETKAER 138
 Db 120 LTFSQHVRCECRPRERKMER 141

RESULT 14
 US-08-795-430-55
 ; Sequence 55, Application US/08795430
 ; Patent No. 6130071

GENERAL INFORMATION:
 ; APPLICANT: Alitalo, Kari
 ; APPLICANT: Joukov, Vladimir
 ; TITLE OF INVENTION: Vascular Endothelial Growth Factor C (VEGF-C)
 ; NUMBER OF SEQUENCES: 57
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
 ; STREET: 6300 Sears Tower, 233 South Wacker Drive
 ; CITY: Chicago
 ; STATE: Illinois
 ; COUNTRY: United States of America
 ; ZIP: 60606-6402

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/795,430
 FILING DATE:
 CLASSIFICATION: 435

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/FI96/00427
 FILING DATE: 01-AUG-1996
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/671,573
 FILING DATE: 28-JUN-1996
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/601,132
 FILING DATE: 14-FEB-1996
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/585,895
 FILING DATE: 12-JAN-1996
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/510,133
 FILING DATE: 01-AUG-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/340,011
 FILING DATE: 14-NOV-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Gass, David A.
 REGISTRATION NUMBER: 38,153
 REFERENCE/DOCKET NUMBER: 28967/33691
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 312/474-6300
 TELEX: 312/474-0448
 TELEX: 25-3856
 INFORMATION FOR SEQ ID NO: 55:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 149 amino acids
 TYPE: amino acid
 STRANDEDNESS: not relevant
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-795-430-55

Query Match Score 474.5; DB 3; Length 149;
 Best Local Similarity 64.1%; Pred. No. 1.4e-47;
 Matches 91; Conservative 19; Mismatches 27; Indels 5; Gaps 2;

Qy 1 MLANKLFTFLQLAGLAVHS---QGALISAGNSTMENVVPNEWGRSICRPMELVY 56
 Db 1 MPYWRLLFPFLQLAGLAVPAVPPQQWALASAGNSSEEVVVFQEVMGRSYCRALERLVD 60

Qy 57 IADEHPNEYSHIFSPSCVLLSRCSGCCGDBGLHCVALKTANITMQLIKPPNNDPHSYVE 116
 Db 61 VVSEYPSEVEHMFSPSCVLLSRCSGCCGDBGLHCVALKTANITMQLIKPPNNDPHSYVE 119

Qy 61 VVSEYPSEVEHMFSPSCVLLSRCSGCCGDBGLHCVALKTANITMQLIKPPNNDPHSYVE 119

Db 61 VVSEYPSEVEHMFSPSCVLLSRCSGCCGDBGLHCVALKTANITMQLIKPPNNDPHSYVE 119

RESULT 15
 US-08-586-039B-47
 ; Sequence 47, Application US/08586039B
 ; Patent No. 6140073
 ; GENERAL INFORMATION:
 ; APPLICANT: Bayne, Marvin L.
 ; APPLICANT: Thomas Jr., Kenneth A.
 ; TITLE OF INVENTION: VASCULAR ENDOTHELIAL CELL GROWTH FACTOR C
 ; TITLE OF INVENTION: SUBUNIT
 ; NUMBER OF SEQUENCES: 49
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Merck & Co., Inc.
 ; STREET: 126 E. Lincoln Avenue
 ; CITY: Rahway
 ; STATE: New Jersey
 ; COUNTRY: USA
 ; ZIP: 07065-0900
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/795,430
 ; FILING DATE:
 ; CLASSIFICATION: 435

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; SOFTWARE: Microsoft Word 6
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/586,039B
; FILING DATE: 16-JAN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/124,259
; FILING DATE: 20-SEP-1993
; APPLICATION NUMBER: 07/676,436
; FILING DATE: 20-MAR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Hand, J. Mark
; REGISTRATION NUMBER: 36,545
; REFERENCE/DOCKET NUMBER: 18361DA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 594-3905
; TELEFAX: (908) 594-4720
; INFORMATION FOR SEQ ID NO: 47:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 149 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: Linear
; MOLECULE TYPE: protein
; US-08-586-039B-47

Qy      Query Match      56.1%; Score 474.5; DB 3; Length 149;
Db      Best Local Similarity 64.1%; Pred. No. 1.e-47; Indels 5; Gaps 2;
       Matches 91; Conservative 19; Mismatches 27; Mismatches 27;

Qy      1 MIAAMKLFPCFLQLAGLAHVS---QGALSAGNNSTENVVPPNEWGRSYCRPMEKVY 56
Db      1 MPYMRLLFPCFLQLAGLAHLPAPPQQWALASAGNSSETVVPFQBTWGRSYCRALERIVD 60
Qy      57 IADEHPNRYSHITFSPSCVILSRCSGCCDEGLHCVALKTANITMQLIKIPPNRDPHSYVE 116
Db      61 VVEYPSSEAHMSPSCVSLRGTGCCDENLHCVPVETANTVMQLIKRSGBDRP-SYVE 119
Qy      117 MTSQDVTCCECRPILETTKAER 138
Db      120 LTPSQHYRCERPLREXMKPER 141

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Search completed: September 13, 2004, 09:54:49
 Job time : 33 secs

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OM protein - protein search, using sw model

Run on: September 13, 2004, 09:53:35 ; Search time 127 Seconds
(without alignments)

398.968 Million cell updates/sec

Title: US-10-071-370A-4

Perfect score: 846

Sequence: 1 MLLAMKLFITCFLQVLAGLAVH.....RKTGKRKQSCKTPQTEPHL 158

Scoring table: BLOSUM62

Gapext 0.0 , Gapext 0.5

Searched: 1335176 seqs, 320689617 residues

Total number of hits satisfying chosen parameters: 1335176

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Published_Applications_AA:
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2: /cgxn2_6_ptodata/2/pubpaa/US05_PUBCOMB.pep:
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4: /cgxn2_6_ptodata/2/pubpaa/US05_PUBCOMB.pep:
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11: /cgxn2_6_ptodata/2/pubpaa/US09C_PUBCOMB.pep:
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16: /cgxn2_6_ptodata/2/pubpaa/US10_NEW_PUB.PEP:
17: /cgxn2_6_ptodata/2/pubpaa/US60_NEW_PUB.PEP:
18: /cgxn2_6_ptodata/2/pubpaa/US60_PUBCOMB.pep:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	846	100.0	158 14	US-10-071-370A-4
2	740	87.5	138 14	US-10-071-370A-6
3	499.5	59.0	170 9	US-09-852-209A-9
4	499.5	59.0	170 12	US-10-439-337A-9
5	499.5	59.0	170 12	US-10-303-997B-9
6	499.5	59.0	170 12	US-10-352-153-5
7	499.5	59.0	170 14	US-10-131-600-9
8	474.5	56.1	149 9	US-09-795-06A-115
9	474.5	56.1	149 12	US-10-211-462-115
10	474.5	56.1	149 14	US-10-386-55
11	474.5	56.1	149 14	US-10-262-538-28
12	474.5	56.1	149 14	US-10-021-660-102
13	474.5	56.1	149 14	US-10-346-802-5
14	474.5	56.1	149 15	US-10-116-275-226
15	450.5	53.3	221 15	US-10-440-464-128

ALIGNMENTS

RESULT 1	US-10-071-370A-4	Publication US/10071370A	GENERAL INFORMATION:
		; Publication No. US2003004571A1	; APPLICANT: Payne, Marvin L.
			; APPLICANT: Conn, Gregory L.
			; APPLICANT: Thomas, Jr., Kenneth A.
			; TITLE OF INVENTION: VASCULAR ENDOTHELIAL CELL GROWTH FACTOR
			; TITLE OF INVENTION: II
			; FILE REFERENCE: 1-B99CB
			; CURRENT APPLICATION NUMBER: US/10/071,370A
			; CURRENT FILING DATE: 2002-02-08
			; PRIOR APPLICATION NUMBER: 09/326,879
			; PRIOR FILING DATE: 1999-06-07
			; PRIOR APPLICATION NUMBER: 09/038,199
			; PRIOR FILING DATE: 1998-03-10
			; PRIOR APPLICATION NUMBER: 09/299,185
			; PRIOR FILING DATE: 1994-08-31
			; SOFTWARE: FastSeq For Windows Version 4.0
			; SEQ ID NO 4
			; LENGTH: 158
			; TYPE: PRT
			; ORGANISM: rat
			; PRIOR APPLICATION NUMBER: 07/586,638
			; PRIOR FILING DATE: 1990-09-21
			; QUERY MATCHES: 158
			; NUMBER OF SEQ ID NOS: 29
			; Best Local Similarity: 100.0%
			; Mismatches: 0;
			; Indels: 0;
			; Gaps: 0;

Qy 1 MLLAMKLFITCFLQVLAGLAVHSGQLSAGNNSTEMEV2PNEWGRSYCRPMEKLYIADE 60
Db 1 MLLAMKLFITCFLQVLAGLAVHSGQLSAGNNSTEMEV2PNEWGRSYCRPMEKLYIADE 60

Qy 61 HPNEVSHIFSPSCVYLSSRCGCGCDEGLHCVALKTANTMQLIKIPRNDRPHSYVYNTFS 120
 Db 61 HPNEVSHIFSPSCVYLSSRCGCGCDEGLHCVALKTANTMQLIKIPRNDRPHSYVYNTFS 120

Qy 121 QDVLCERCPILETTKAERRRKTKGKRSKTPQTEBPHL 158
 Db 121 QDVLCERCPILETTKAERRRKTKGKRSKTPQTEBPHL 158

RESULT 2
 US-10-071-370A-6
 ; Sequence 6, Application US/10071370A
 ; Publication No. US20030045471A1
 ; GENERAL INFORMATION;
 ; APPLICANT: Bayne, Marvin L.
 ; APPLICANT: Conn, Gregory L.
 ; APPLICANT: Thomas, Jr., Kenneth A.
 ; TITLE OF INVENTION: VASCULAR ENDOTHELIAL CELL GROWTH FACTOR
 ; FILE REFERENCE: 18199CB
 ; CURRENT APPLICATION NUMBER: US/10/071,370A
 ; CURRENT FILING DATE: 2002-02-08
 ; PRIOR APPLICATION NUMBER: 09/326,879
 ; PRIOR FILING DATE: 1999-06-07
 ; PRIOR APPLICATION NUMBER: 09/038,199
 ; PRIOR FILING DATE: 1998-03-10
 ; PRIOR FILING NUMBER: 08/299,185
 ; PRIOR FILING DATE: 1994-08-31
 ; PRIOR APPLICATION NUMBER: 08/000,834
 ; PRIOR FILING DATE: 1993-01-05
 ; PRIOR APPLICATION NUMBER: 07/586,638
 ; PRIOR FILING DATE: 1990-09-21
 ; NUMBER OF SEQ ID NOS: 29
 ; SOFTWARE: FastSEQ For Windows Version 4.0
 ; SEQ ID NO 6
 ; LENGTH: 138
 ; TYPE: PRT
 ; ORGANISM: rat
 ; US-10-071-370A-6

Query Match 87.5%; Score 740; DB 14; Length 138;
 Best Local Similarity 100.0%; Pred. No. 3.e-72;
 Matches 138; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MIAANKLFTCFLQVLAGLAVHS---QGALSAGNNSTEMEVPPNENWGRSYCRPMELVY 56
 Db 1 MPYMLFLFCFLQVLAGLALPAVPPQWALSAGNGSEVEVVPQEYNGRSYCRALRLVD 60

Qy 57 IADBPNEVSHIFSPCVLSSRSGCCGDEGLHCVALKTANTMQLKIPRNDRPHSYVVE 116
 Db 61 VNSEYPSEVENHMSPSCVSLRCTGCCGDEDLHCVPVETANTMQLKIRSGDR-SYVE 119

Qy 117 MTFSQDVLCERCPILETTKAERRRKTKGKRSKTPQ 152
 Db 120 LTFSQHVRCECRBLREKMPKPERRPGKGKRRRENO 155

RESULT 4

US-10-43-337A-9
 ; Sequence 9, Application US/10439337A
 ; Publication No. US20040053837A1
 ; GENERAL INFORMATION;
 ; APPLICANT: Li, Xuri
 ; APPLICANT: ERIKSSON, Ulf
 ; APPLICANT: CARMELLET, Peter
 ; APPLICANT: COLIJUM, Desire
 ; TITLE OF INVENTION: ANGIOGENESIS
 ; FILE REFERENCE: 029065_447404
 ; CURRENT APPLICATION NUMBER: US/10/439,337A
 ; CURRENT FILING DATE: 2003-05-16
 ; PRIOR APPLICATION NUMBER: US 10/303,997
 ; PRIOR FILING DATE: 2002-11-26
 ; PRIOR APPLICATION NUMBER: US 09/410,349
 ; PRIOR FILING DATE: 1999-09-30
 ; PRIOR APPLICATION NUMBER: US 60/102,461
 ; PRIOR FILING DATE: 1998-09-30
 ; PRIOR APPLICATION NUMBER: US 60/108,109
 ; PRIOR FILING DATE: 1998-11-12
 ; PRIOR APPLICATION NUMBER: US 60/110,749
 ; PRIOR FILING DATE: 1998-12-03
 ; PRIOR APPLICATION NUMBER: US 60/113,002
 ; PRIOR FILING DATE: 1998-12-18
 ; PRIOR APPLICATION NUMBER: US 60/135,426
 ; PRIOR FILING DATE: 1999-05-21
 ; PRIOR APPLICATION NUMBER: US 60/144,022
 ; PRIOR FILING DATE: 1999-07-15
 ; NUMBER OF SEQ ID NOS: 40
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 9
 ; LENGTH: 170

Query Match 59.0%; Score 499.5; DB 9;
 Best Local Similarity 61.5%; Pred. No. 5.e-46;
 Matches 96; Conservative 23; Mismatches 32; Indels 5; Gaps 2;

Qy 1 MIAANKLFTCFLQVLAGLAVHS---QGALSAGNNSTEMEVPPNENWGRSYCRPMELVY 56
 Db 1 MPYMLFLFCFLQVLAGLALPAVPPQWALSAGNGSEVEVVPQEYNGRSYCRALRLVD 60

Qy 57 IADBPNEVSHIFSPCVLSSRSGCCGDEGLHCVALKTANTMQLKIPRNDRPHSYVVE 116
 Db 61 VNSEYPSEVENHMSPSCVSLRCTGCCGDEDLHCVPVETANTMQLKIRSGDR-SYVE 119

Qy 117 MTFSQDVLCERCPILETTKAERRRKTKGKRSKTPQ 152
 Db 120 LTFSQHVRCECRBLREKMPKPERRPGKGKRRRENO 155

TYPE: PRT ; ORGANISM: Homo sapiens
 US-10-439-37A-9

Query Match 59.0%; Score 499.5; DB 12; Length 170;
 Best Local Similarity 61.5%; Pred. No. 5.6e-46;
 Matches 96; Conservative 23; Mismatches 32; Indels 5; Gaps 2;

Qy 1 MLAMKLFCTFLQVLAGLAVHS---QGALSAGINNSTEMEVVPNEWGRSVCRCRPMELVY 56
 Db 1 MPVNRLLFPFLQVLAGLAVHS---QGALSAGINNSTEMEVVPNEWGRSVCRCRPMELVY 60

Qy 57 IADEHPNEVSHIFSPSCVILSRSGCCDGEGLCYALKTANITMQLKIPPNRDPHSYVE 116
 Db 61 VVSEYPSEVEHMSPSCVSLRCTGCCDDELHCVPETANTMQLKIRSGDRP-SYVE 119

Qy 117 MTFSDQVLCECRPILETTKAERRTKKGKQSKTPQ 152
 Db 120 LTFSQHVRCERPILETTKAERRTKKGKQRRRRENQ 155

RESULT 5
 US-10-303-997B-9
 ; Sequence 9, Application US/10303997B
 ; Publication No. US20030211994A1
 ; GENERAL INFORMATION:
 ; APPLICANT: LI, Xuri
 ; APPLICANT: ERIKSSON, Ulle
 ; APPLICANT: CARMELLET, Desire
 ; TITLE OF INVENTION: COMPOSITION AND METHOD FOR MODULATING VASCULOGENESIS AND ANGIOGEN
 ; CURRENT APPLICATION NUMBER: US/10/303,997B
 ; CURRENT FILING DATE: 2002-11-26
 ; PRIOR APPLICATION NUMBER: US 09/410,349
 ; PRIOR FILING DATE: 1999-09-30
 ; PRIOR APPLICATION NUMBER: US 60/102,461
 ; PRIOR FILING DATE: 1998-09-30
 ; PRIOR APPLICATION NUMBER: US 60/108,109
 ; PRIOR FILING DATE: 1998-11-12
 ; PRIOR APPLICATION NUMBER: US 60/110,749
 ; PRIOR APPLICATION NUMBER: US 60/113,002
 ; PRIOR FILING DATE: 1998-12-18
 ; PRIOR APPLICATION NUMBER: US 60/135,426
 ; PRIOR FILING DATE: 1999-05-21
 ; PRIOR APPLICATION NUMBER: US 60/144,022
 ; PRIOR FILING DATE: 1999-07-15
 ; NUMBER OF SEQ ID NOS: 40
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO: 9

Query Match 59.0%; Score 499.5; DB 12; Length 170;
 Best Local Similarity 61.5%; Pred. No. 5.6e-46;
 Matches 96; Conservative 23; Mismatches 32; Indels 5; Gaps 2;

Qy 1 MLAMKLFCTFLQVLAGLAVHS---QGALSAGINNSTEMEVVPNEWGRSVCRCRPMELVY 56
 Db 1 MPVNRLLFPFLQVLAGLAVHS---QGALSAGINNSTEMEVVPNEWGRSVCRCRPMELVY 60

Qy 57 IADEHPNEVSHIFSPSCVILSRSGCCDGEGLCYALKTANITMQLKIPPNRDPHSYVE 116
 Db 61 VVSEYPSEVEHMSPSCVSLRCTGCCDDELHCVPETANTMQLKIRSGDRP-SYVE 119

Qy 117 MTFSDQVLCECRPILETTKAERRTKKGKQSKTPQ 152
 Db 120 LTFSQHVRCERPILETTKAERRTKKGKQRRRRENQ 155

RESULT 6
 US-10-352-153-5
 ; Sequence 5, Application US/10352153
 ; Publication No. US200302110A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wise, Lyn M
 ; APPLICANT: Mercer, Andrew A
 ; APPLICANT: Savory, Loreen J
 ; APPLICANT: Fleming, Stephen B
 ; APPLICANT: Stracker, Stephen
 ; TITLE OF INVENTION: VASCULAR ENDOOTHELIAL GROWTH FACTOR-LIKE PROTEIN FROM ORF
 ; TITLE OF INVENTION: VIRUS NF2 BINDS AND ACTIVATES MAMMALIAN VEGF
 ; TITLE OF INVENTION: RECEPTOR-2, AND USES THEREOF
 ; FILE REFERENCE: Sequence Listing for 09/431,833
 ; CURRENT APPLICATION NUMBER: US/10/352,153
 ; CURRENT FILING DATE: 2003-01-28
 ; PRIOR APPLICATION NUMBER: US/09/431,888A
 ; PRIOR FILING DATE: 1999-11-02
 ; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/106,689
 ; PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-02
 ; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/106,800
 ; PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-03
 ; NUMBER OF SEQ ID NOS: 11
 ; SEQ ID NO: 5
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; LENGTH: 170

Query Match 59.0%; Score 499.5; DB 12; Length 170;
 Best Local Similarity 61.5%; Pred. No. 5.6e-46;
 Matches 96; Conservative 23; Mismatches 32; Indels 5; Gaps 2;

Qy 1 MLAMKLFCTFLQVLAGLAVHS---QGALSAGINNSTEMEVVPNEWGRSVCRCRPMELVY 56
 Db 1 MPVNRLLFPFLQVLAGLAVHS---QGALSAGINNSTEMEVVPNEWGRSVCRCRPMELVY 60

Qy 57 IADEHPNEVSHIFSPSCVILSRSGCCDGEGLCYALKTANITMQLKIPPNRDPHSYVE 116
 Db 61 VVSEYPSEVEHMSPSCVSLRCTGCCDDELHCVPETANTMQLKIRSGDRP-SYVE 119

Qy 117 MTFSDQVLCECRPILETTKAERRTKKGKQSKTPQ 152
 Db 120 LTFSQHVRCERPILETTKAERRTKKGKQRRRRENQ 155

RESULT 7
 US-10-131-600-9
 ; Sequence 9, Application US/10131600
 ; Publication No. US20030082670A1
 ; GENERAL INFORMATION:
 ; APPLICANT: ERIKSSON, Ulle
 ; APPLICANT: AASE, Karin
 ; APPLICANT: LEE, Xuri
 ; APPLICANT: PONTEN, Annica
 ; APPLICANT: UUTELA, Marko
 ; APPLICANT: OESTMAN, Arne
 ; APPLICANT: HELDMAN, Carl-Henrik
 ; APPLICANT: BETSHOLTZ, Christian
 ; TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR C, DNA CODING
 ; TITLE OF INVENTION: THEREFOR, AND USES THEREOF
 ; CURRENT APPLICATION NUMBER: 09-10349-Eriksson et al-1064-44/40
 ; CURRENT FILING DATE: 2002-04-25
 ; PRIOR APPLICATION NUMBER: US/10/131,600
 ; PRIOR FILING DATE: 1999-09-30
 ; PRIOR APPLICATION NUMBER: 60/108,109
 ; PRIOR FILING DATE: 1998-11-12
 ; PRIOR APPLICATION NUMBER: 60/110,749
 ; PRIOR FILING DATE: 1998-12-03
 ; PRIOR APPLICATION NUMBER: 60/113,002
 ; PRIOR FILING DATE: 1998-12-18
 ; PRIOR APPLICATION NUMBER: US 60/135,426

PRIOR FILING DATE: 1998-12-18
 PRIOR APPLICATION NUMBER: 60/135,426
 PRIOR FILING DATE: 1999-05-21
 PRIOR APPLICATION NUMBER: 60/144,022
 PRIOR FILING DATE: 1999-07-15
 NUMBER OF SEQ ID NOS: 39
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO: 9
 LENGTH: 170
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-131-600-9

Query Match 59.0%; Score 499.5; DB 14; Length 170;
 Best Local Similarity 61.5%; Pred. No. 5.6e-46;
 Matches 23; Mismatches 32; Indels 5; Gaps 2;

Qy 1 MLANKLFTCFQLQVLAGIAVHS---QGALSAGNSTMENVVPPNEVWGRSYCPMEKLVY 56
 Db 1 MPYMRLLFPCFLQVLAGIAVHS---QGALSAGNSTMENVVPPNEVWGRSYCPMEKLVY 56

Qy 57 IADBHPNVSHIFSPSCVLLSRSGCCDEGHCVALKTANITMQLIKIPPNRDPHSEYVE 116
 Db 61 VISEYPSSEVAMSPSCVLLRGCQDDEHLICVPTVANITMQLIKRSGDRP-SYVE 119

Qy 117 MTFSDQDVLCRCPLETTKAERRTKGKRQSKTPQ 152
 Db 120 LTFSQHYRECECRPLREKMKPERPKGRGKRRRRENQ 155

Query Match 56.1%; Score 474.5; DB 12; Length 149;
 Best Local Similarity 64.1%; Pred. No. 2.5e-43;
 Matches 91; Conservative 19; Mismatches 27; Indels 5; Gaps 2;

Qy 1 MLANKLFTCFQLQVLAGIAVHS---QGALSAGNSTMENVVPPNEVWGRSYCPMEKLVY 56
 Db 1 MPYMRLLFPCFLQVLAGIAVHS---QGALSAGNSTMENVVPPNEVWGRSYCPMEKLVY 56

Qy 57 IADBHPNVSHIFSPSCVLLSRSGCCDEGHCVALKTANITMQLIKIPPNRDPHSEYVE 116
 Db 61 VISEYPSSEVAMSPSCVLLRGCQDDEHLICVPTVANITMQLIKRSGDRP-SYVE 119

Qy 117 MTFSDQDVLCRCPLETTKAERRTKGKRQSKTPQ 138
 Db 120 LTFSQHYRECECRPLREKMKPER 141

RESULT 10
 US-10-201-386-55
 Sequence 55, Application US/10201386
 ; GENERAL INFORMATION:
 ; Patent No. US20030091567A1
 ; APPLICANT: Altitlo et al.
 ; TITLE OF INVENTION: ENDOTHELIAL GROWTH HYBRID VASCULAR
 ; FILE REFERENCE: 28367/35977B
 ; CURRENT FILING DATE: 2001-02-26
 ; PRIOR APPLICATION NUMBER: US/09/795,006A
 ; PRIOR FILING DATE: 2000-05-18
 ; PRIOR APPLICATION NUMBER: US/09/185,205
 ; PRIOR FILING DATE: 2000-02-25
 ; NUMBER OF SEQ ID NOS: 175
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO: 115
 ; LENGTH: 149
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-795-006A-115

Query Match 56.1%; Score 474.5; DB 9; Length 149;
 Best Local Similarity 64.1%; Pred. No. 2.5e-43;
 Matches 91; Conservative 19; Mismatches 27; Indels 5; Gaps 2;

Qy 1 MLANKLFTCFQLQVLAGIAVHS---QGALSAGNSTMENVVPPNEVWGRSYCPMEKLVY 56
 Db 1 MPYMRLLFPCFLQVLAGIAVHS---QGALSAGNSTMENVVPPNEVWGRSYCPMEKLVY 56

Qy 57 IADBHPNVSHIFSPSCVLLSRSGCCDEGHCVALKTANITMQLIKIPPNRDPHSEYVE 116
 Db 61 VISEYPSSEVAMSPSCVLLRGCQDDEHLICVPTVANITMQLIKRSGDRP-SYVE 119

Qy 117 MTFSDQDVLCRCPLETTKAERRTKGKRQSKTPQ 138
 Db 120 LTFSQHYRECECRPLREKMKPER 141

RESULT 9
 US-10-211-462-115
 ; Sequence 115, Application US/10211462

Page 5

Qy 57 IADEHPNEVSHIFSPSCVLLSRSGCGDEGLHCVALKTANITMQLIKTPPNRDPHSYVE 116 ; PRIORITY FILING DATE: 2003-02-24
 :
 Db 61 VVSEYSPSEEHMFSPSCVLLRCGCGDENLHCVPVETANVMTQLIKRSGDRP-SYVE 119 ; NUMBER OF SEQ ID NOS: 185
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO: 128
 ; LENGTH: 221
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-10-440-464-128

Query Match 53.3%; Score 450.5; DB 15; Length 221;
 Best Local Similarity 65.2%; Pred. No. 1.7e-40;
 Matches 86; Conservative 18; Mismatches 23; Indels 5; Gaps 2;

Qy 1 MLANKLIFTFLQVLAGLAHVS---OGLASAGNNSTMEVVPFNEYWGRSYCRPMELKLVY 56
 Db 1 MPVNRLLPFCLQLAGLALPAVPQQWALSAGNGSSBVEVPPQEWGRSYCRALERLVD 60

Qy 57 IADEHPNEVSHIFSPSCVLLSRSGCGDEGLHCVALKTANITMQLIKPPNRPDSYVE 116
 Db 61 VVSEYSPSEEHMFSPSCVLLRCGCGDENLHCVPVETANVMTQLIKRSGDRP-SYVE 119

Search completed: September 13, 2004, 10:05:10
 Job time : 128 sec₆

RESULT 14
 US-10-116-275-226
 ; Sequence 226, Application US/10116275
 ; PUBLICATION NO. US20030211476A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Elan Pharmaceutical Technology
 ; APPLICANT: O'Mahony, Daniel J.
 ; APPLICANT: Brayden, David
 ; APPLICANT: Byrne, Daragh
 ; APPLICANT: Lambkin, Imelda
 ; APPLICANT: Higgins, Lisa
 ; TITLE OF INVENTION: Genetic Analysis of Peyer's Patches and M Cells and Methods and
 ; FILE REFERENCE: E1067/20087
 ; CURRENT APPLICATION NUMBER: US/10/116,275
 ; CURRENT FILING DATE: 2002-10-04
 ; NUMBER OF SEQ ID NOS: 349
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO: 226
 ; LENGTH: 149
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-10-116-275-226

Query Match 56.1%; Score 474.5; DB 15; Length 149;
 Best Local Similarity 64.1%; Pred. No. 2.5e-43; Mismatches 27; Indels 5; Gaps 2;

Qy 1 MLANKLIFTFLQVLAGLAHVS---OGLASAGNNSTMEVVPFNEYWGRSYCRPMELKLVY 56
 Db 1 MPVNRLLPFCLQLAGLALPAVPQQWALSAGNGSSBVEVPPQEWGRSYCRALERLVD 60

Qy 57 IADEHPNEVSHIFSPSCVLLSRSGCGDEGLHCVALKTANITMQLIKPPNRPDSYVE 116
 Db 61 VVSEYSPSEEHMFSPSCVLLRCGCGDENLHCVPVETANVMTQLIKRSGDRP-SYVE 119

Qy 117 MTFSQDVLICECPFILETTKAER 138
 Db 120 LTFSQHYRCRPLREMKPER 141

RESULT 15
 US-10-440-464-128
 ; Sequence 128, Application US/10440464
 ; PUBLICATION NO. US20040018528A1
 ; GENERAL INFORMATION:
 ; APPLICANT: DEPRIMO, SAMUEL
 ; APPLICANT: O'FARRELL, ANNE-MARIE
 ; APPLICANT: MORIMOTO, MIYSSA
 ; APPLICANT: SMOLICH, BEVERLY
 ; APPLICANT: MANNING, WILLIAM
 ; APPLICANT: WALTER, SARAH
 ; APPLICANT: CHERKINGTON, JULIE
 ; APPLICANT: SCHILLING, JIM
 ; TITLE OF INVENTION: NOVEL BIOMARKERS OF TYROSINE KINASE INHIBITOR EXPOSURE
 ; TITLE OF INVENTION: AND ACTIVITY IN MAMMALS
 ; FILE REFERENCE: 038602/1592
 ; CURRENT APPLICATION NUMBER: US/10/440,464
 ; CURRENT FILING DATE: 2003-05-19
 ; PRIOR APPLICATION NUMBER: 60/380,872
 ; PRIOR FILING DATE: 2002-05-17
 ; PRIOR APPLICATION NUMBER: 60/448,922
 ; PRIOR FILING DATE: 2003-02-24
 ; PRIOR APPLICATION NUMBER: 60/448,874

US-10-071-370A-4											
Perfect score:		946									
Sequence:		MLANKLFTCFQLVLAGLAHV.....RKTGSKRKRSQSKTPQTTEPHL 158									
Scoring table:		BLOSUM62									
Gapopen:		10.0 , Gapext: 0.5									
Searched:		141681 seqs, 52070155 residues									
Total number of hits satisfying chosen parameters:		141681									
Minimum DB seq length: 0 Maximum DB seq length: 2000000000											
Post-Processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries											
Database : SwissProt_42;*											
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.											
SUMMARIES											
Result No.	Score	Query Match Length	DB ID	Description							
1	846	100.0	158	PLGF RAT							
2	785	92.8	158	PLGF MOUSE							
3	450.5	53.3	221	PLGF HUMAN							
4	426.5	50.4	149	PLGF BOVIN							
5	322.5	38.1	144	VEGA_CANPA							
6	320.5	37.9	214	VEGA_MOUSE							
7	319.5	37.8	214	VEGA RAT							
8	315	37.2	222	VEGA_HUMAN							
9	296.5	35.0	190	VEGA_PIG							
10	294.5	34.8	190	VEGA_HORSE							
11	291.5	34.5	216	VEGA_CHICK							
12	283.5	33.5	190	VEGA_BOVIN							
13	282.5	33.4	190	VEGA_MESAU							
14	282	33.3	146	VEGA_SHEEP							
15	280.5	33.2	164	VEGA_CAVPO							
16	189	22.3	133	VEGH_ORFN2							
17	188	22.2	207	VEGB_MOUSE							
18	182	21.5	207	VEGB_HUMAN							
19	179.5	21.2	207	VEGB_BOVIN							
20	179	21.1	135	VEGB RAT							
21	174	20.6	358	VEGD MOUSE							
22	167	19.7	148	VEGH_ORFN7							
23	158	18.7	354	VEGD_HUMAN							
24	153	18.1	326	VEGD RAT							
25	144	17.0	419	VEGC_HUMAN							
26	140	16.5	415	VEGC MOUSE							
27	114	13.5	221	PDGB RAT							
28	112	13.2	241	PDGB MOUSE							
29	110	13.0	245	PDGB_FELCA							
30	108	12.8	241	PDGB_HUMAN							
31	105.5	12.5	241	PDGB_SHEEP							
32	99.5	11.4	226	PDGB_SMRSAV							
33	96.5	11.4	226	TSTS_SMSAV							

34	94.5	11.2	211	1	PDGA- <u>MOUSE</u>	P20033	mus musculus
35	92.5	10.9	204	1	PDGA- <u>RAT</u>	P28576	rattus norv
36	89.5	10.6	211	1	PDGA- <u>HUMAN</u>	P04085	homo sapien
37	88.5	10.5	126	1	VEGC- <u>RAT</u>	Q35757	rattus norv
38	83	9.8	226	1	PDGA- <u>HUMAN</u>	P13698	stomoxys lae
39	81	9.6	607	1	THEA- <u>HUMAN</u>	Q8wxia	homo sapien
40	77.5	9.2	326	1	Y338- <u>CHLMU</u>	Q9pkx2	chlamydia m
41	77	9.1	1	GLHA- <u>ACALA</u>	P30970	acanthamoebagr	
42	77	9.1	420	1	VIT3- <u>DROME</u>	P06607	drosophila
43	75	8.9	731	1	DAXX- <u>RAT</u>	Q8vib2	rattus norv
44	74	8.8	150	1	R142- <u>MAIZE</u>	P19951	zea mays (m
45	74.5	8.8	153	1	RS14- <u>CHLRE</u>	P46295	chlamydomon

ALIGNMENTS

searched: 141681 seqs, 52070155 residues
 total number of hits satisfying chosen parameters: 141681
 minimum DB seq length: 0
 maximum DB seq length: 200000000
 post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing First 45 summaries
 SwissProt 42.*
 +base : NCBI TaxID:10116
 PLGF_BAT ID PLGF-BAT STANDARD; PRT; 158 AA.
 AC Q63434; DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Placenta growth factor precursor (PIGF).
 PLGF GN Rat
 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus;
 Rattus norvegicus (Rat)

RP SEQUENCE FROM N.A. (ISOFORM PLGF-3).
 RC TISSUE=Placenta;
 RX MEDLINE=97350807; PubMed=9207183;
 RA Cao Y., Ji W.-R., Qi P., Rosin A., Cao Y.; "Placenta growth factor: identification and characterization of a novel isoform generated by RNA alternative splicing.";
 RT RT novel isoform generated by RNA alternative splicing.";
 RL Biochem. Biophys. Res. Commun. 235:493-498(1997).
 RN [5]
 RP SEQUENCE FROM N.A. (ISOFORM PLGF-1).
 RX PubMed=12508121;
 RA Heilig R., Eckenberg R., Petit J.-L., Bonknechtein N., Da Silva C., Cattolico L., Levy M., Barthe V., De Berardinis V., Ureta-Vidal A., Pelleter V., Anthouard V., Rowen L., Madan A., Qin S., Sun H., Du H., Pepin K., Artiguenave F., Robert C., Cruaud C., Brueis T., Jaillon O., Friedlander L., Samson G., Brottier P., Cure A., Segurens B., Aniere F., Samain S., Crespeau H., Abbasi N., Aich N., Boscus D., Dickhoff R., Dors M., Dubois I., Friedman C., Gouyvenoux M., James R., Madan A., Mairy Estrada B., Mangenot S., Martens N., Menard M., Oztas S., Ratcliffe A., Shaffer T., Trask B., Vacherie B., Bellemare C., Belser C., Besnard-Gonnet M., Bartol-Mavel D., Boutard M., Briez-Silla S., Combette S., Dufosse-Laurent J., Ferron C., Lechaplais C., Louesse C., Muselet D., Magdelanet G., Pateau E., Bluet E., Sirvain-Trukniewicz P., Trybou A., Vega-czarny N., Battaille E., Bluet E., Dubois M., Dumont C., Guerin T., Hafray S., Hammadi R., Muanga J., Pellicoin V., Robert D., Wunderle E., Gauguet G., Roy A., Sainte-Martine L., Verdier J., Verdier-Discalca C., Hillier L.W., Fulton L., McPherson J., Matsuda F., Wilson R., Scarpa C., Gyapay G., Wincker P., Saurin W., Quertier F., Waterston R., Hood L., Weissenbach J.; "The DNA sequence and analysis of human chromosome 14.";
 RA RT Nature 421:601-607(2003).
 RL [6]
 RP SEQUENCE FROM N.A. (ISOFORM PLGF-2).
 RC TISSUE=Muscle, and Placenta;
 RX MEDLINE=1247932; PubMed=1247932;
 RA Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G., Klausner R.D., Feingold E.A., Schuler G.D., Altenschul S.F., Zeeberg B., Buetow K.H., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Maruskin K., Farmer A.A., Rubin G.M., Hong L., Brownstein M.J., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Stapleton M., Soares M.B., Usdin T.B., Toshiyuki S., Carminci P., Prange C., Raha S., Loqueland N.A., Peters G.J., Abramson R.D., Mullally S.J., PAWA S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahy J., Heiton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimeswood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smilus D.E., Scherch A., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
 RT RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [7]
 RP CHARACTERIZATION, AND SEQUENCE OF 19-24.
 RX MEDLINE=7929268; PubMed=7929268;
 RA Park J.E., Chen H.H., Winer J., Houch K.A., Ferrara N.; "Placenta growth factor. Potentiation of vascular endothelial growth factor bioactivity, in vitro and in vivo, and high affinity binding to Flt-1 but not to Flk-1/KDR";
 RT RT J. Biol. Chem. 269:25646-25654(1994).
 RL RN [8]
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) (ISOFORM PLGF-1).
 RX MEDLINE=2192270; PubMed=11069911;
 RA Iyer S., Leonidas D.D., Swaminathan G.J., Maglione D., Battisti M., Tucci M., Persico M.G., Acharya K.R.; "The crystal structure of human placenta growth factor-1 (PLGF-1), an angiogenic protein, at 2.0 Å resolution.";
 RT RT J. Biol. Chem. 276:12153-12161(2001).
 CC CC -!- FUNCTION: Growth factor active in angiogenesis, and endothelial cell growth, stimulating their proliferation and migration. It
 binds to receptor VEGFR-1/FLT1. PLGF-2 binds neuropilin-1 and 2 in a heparin-dependent manner.
 CC -!- SUBUNIT: Antiparallel homodimer; disulfide-linked. Also found as heterodimer with VEGF/VEGFA. PLGF-3 is found both as homodimer and as monomer.
 CC -!- SUBCELLULAR LOCATION: The three forms are secreted but PLGF-2 appears to remain cell attached unless released by heparin.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=3;
 CC Name=PLGF-3;
 CC IsoID=P49763-1; Sequence=Displayed;
 CC Name=PLGF-1; Synonyms=PLGF-131;
 CC IsoID=P49763-2; Sequence=VSP_004644;
 CC Name=PLGF-2; Synonyms=PLGF-152;
 CC IsoID=P49763-3; Sequence=VSP_004644; VSP_004645;
 CC -!- TISSUE SPECIFICITY: While the three forms are present in most placental tissues, the PLGF-2 is specific to early (8 week) placenta and only PLGF-1 is found in the colon and mammary carcinomas.
 CC -!- DOMAIN: PLGF-2 contains a basic insert which acts as a cell retention signal.
 CC -!- PTM: N-glycosylated.
 CC -!- SIMILARITY: Belongs to the PDGF/VEGF growth factor family.
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 CC DR EMBL; X54936; CAA38699.1; -.
 CC DR EMBL; S72960; AA30462.2; -.
 CC DR EMBL; S57152; AB25832.2; ALT SEQ.
 CC DR EMBL; AC00653.0; AAD30179.1; -.
 CC DR EMBL; BC001422; AAH01422.1; -.
 CC DR EMBL; BC007789; AAH07789.1; -.
 CC DR EMBL; BC007255; AAH07255.1; -.
 CC DR PIR; A18411; CAB01393.1; -.
 CC DR PIR; A41236; A41236.
 CC DR PDB; 09-MAY-01.
 CC DR Genbank; HGNC:8893; PGF.
 CC DR MIM; 601121; -.
 CC DR GO; GO:0008083; P: growth factor activity; TAS.
 CC DR GO; GO:0007267; P: cell-cell signaling; TAS.
 CC DR GO; GO:000784; P: positive regulation of cell proliferation; TAS.
 CC DR GO; GO:007165; P: signal transduction; TAS.
 CC DR InterPro; IPR000072; PD_growth_factor.
 CC DR Pfam; PF00341; PGF.
 CC DR PROSITE; PS00249; PDGF_1.
 CC DR PROSITE; PS50278; PDGF_2.
 CC KW Angiogenesis; Mitogen; Growth Factor; Glycoprotein; Signal; Heparin-binding; Alternative splicing; 3D-structure.
 CC FT SIGNAL 1 18
 CC FT CHAIN 19 221 PLACENTA GROWTH FACTOR.
 CC FT DOMAIN 193 213 HEPARIN-BINDING (PROBABLE).
 CC FT DISULFID 52 94 N-LINKED (GLCNAC . .) (POTENTIAL).
 CC FT DISULFID 83 128 N-LINKED (GLCNAC . .) (POTENTIAL).
 CC FT DISULFID 87 130 Missing (in isoform PLGF-1 and isoform PLGF-2).
 CC FT DISULFID 77 77 INTERCHAIN.
 CC FT DISULFID 86 86 N-LINKED (GLCNAC . .) (POTENTIAL).
 CC FT CARBOHYD 33 33 CARBOHYD 33 33
 CC FT CARBOHYD 101 101 VARSPLIC 132 203
 CC FT VARSPLIC 132 203
 CC FT VARSPLIC 213 213
 CC FT CONFLICT 91 91
 CC FT CONFLICT 91 91

CC Name=VEGF-188;
 CC IsoID:Q9MYV3-1; Sequence=Displayed;
 CC
 CC Name=VEGF-182;
 CC IsoID:Q9MYV3-2; Sequence=VSP_004617;
 CC
 CC Name=VEGF-164;
 CC IsoID:Q9MYV3-3; Sequence=VSP_004615; VSP_004616;
 CC -|- SIMILARITY: Belongs to the PDGF/VEGF growth factor family.
 CC
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 CC
 DR AJ133258; CAB82426.1; -;
 DR EMBL; AF133250; AAD29654.1; -;
 DR EMBL; AF133249; AAD29683.1; -;
 DR EMBL; AF133248; AAD29682.1; -;
 DR HSPP; P15692; 1VGH.
 DR InterPro; IPR00072; PD_growth_factor.
 DR PF00341; PDGF; 1.
 DR Prodrom; P001629; PD_growth_factor; 1.
 DR SMART; SMM0141; PDGF; 1.
 DR PROSITE; PS00249; PDGF_1; 1.
 DR PROSITE; PS5027B; PDGF_2; 1.
 KW Mitogen; Angiogenesis; Growth factor; Glycoprotein; Signal;
 KW Heparin-binding; Alternative splicing; Multigene family.
 FT SIGNAL 1 26
 FT CHAIN 27
 FT DISULFID 51
 FT DISULFID 82
 FT DISULFID 86
 FT DISULFID 76
 FT DISULFID 85
 FT CARBOHYD 100
 FT VARSPLIC 140
 FT VARSPLIC 141
 FT VARSPLIC 159
 FT CONFLICT 143
 FT CONFLICT 161
 SQ SEQUENCE 214 AA; 25175 MW; OAC980A158C44B27 CRC34;

Query Match 38.1%; Score 322.5; DB 1; Length 214;
 Best Local Similarity 49.6%; Pred. No. 2.5e-26;
 Matches 64; Conservative 18; Mismatches 46; Indels 1; Gaps 1;

Qy 21 SGCGDEGLHCAVLTANITMQLKIPNNPDRPHSYVEMMFSQDVLCECPILETTKAERRK 140
 Db 84 GCQNDEGIECVPTSEFNITMQMIRKICRPKHQGQH-TGEMSFLQHSKCECRPKDQRQERKS 142

Qy 81 GCGCDEGLHCAVLTANITMQLKIPNNPDRPHSYVEMMFSQDVLCECPILETTKAERRK 140
 ID 84 GCQNDEGIECVPTSEFNITMQMIRKICRPKHQGQH-TGEMSFLQHSKCECRPKDQRQERKS 142

Qy 141 TKGKRKQSK 149
 Db 143 IRGKGKGOK 151

RESULT 6
 VEGA_MOUSE STANDARD; PRT; 214 AA.
 AC Q00731; ID VEGA_MOUSE STANDARD; PRT; 214 AA.
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Vascular endothelial growth factor A precursor (VEGF-A) (vascular
 DE permeability factor) (VPF).

GN VEGF OR VEGFA;
 OS Mus musculus (Mouse).
 OC Lukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORMS VEGF-1; VEGF-2 AND VEGF-3).
 RX MEDLINE:92274860; PubMed=152003;
 RA Breier G.; Albrecht U.; Starrer S.; Risau W.;
 RT "Expression of vascular endothelial growth factor during embryonic
 RT angiogenesis and endothelial cell differentiation." Development 114:521-532(1992).
 RL J. Biol. Chem. 267:16317-16322(1992).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM VEGF-1).
 RX MEDLINE:92355593; PubMed=164816;
 RA Claffey K.P.; Wilkison W.O.; Spiegelman B.M.;
 RT "vascular endothelial growth factor. Regulation by cell
 differentiation and activated second messenger pathways." J. Biol. Chem. 267:16317-16322(1992).
 RN [3]
 RP SEQUENCE OF 1-3 FROM N.A.
 RX MEDLINE:96216498; PubMed=8632007;
 RA Shima D.T.; Kuroki M.; Deutsch U.; Ng Y.; Adams A.P.; D'Amore P.A.;
 RT "The mouse gene for vascular endothelial growth factor. Genomic
 structure, definition of the transcriptional unit and
 characterization of transcriptional and post-transcriptional
 regulatory sequences." J. Biol. Chem. 271:3877-3883(1996).
 CC -|- FUNCTION: Growth factor active in angiogenesis, vasculogenesis and
 CC endothelial cell growth. It induces endothelial cell
 CC proliferation, promotes cell migration, inhibits apoptosis, and
 CC induces permeabilization of blood vessels. It binds to the
 CC VEGFR1/FIT-1 and VEGFR2/Kdr receptors and to heparan sulfate and
 CC heparin (By similarity).
 CC -|- SUBUNIT: Homodimer; disulfide-linked. Also found as heterodimer
 CC with PIGF (By similarity).
 CC -|- SUBCELLULAR LOCATION: VEGF-1 and VEGF-2 are secreted while VEGF-3
 CC remains cell surface associated unless released by heparin.
 CC -|- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=3;
 CC Name=VEGF-3; Synonyms=VEGF188;
 CC IsoID=Q00731-1; Sequence=Displayed;
 CC Name=VEGF-1; Synonyms=VEGF164;
 CC IsoID=Q00731-2; Sequence=VSP_004626; VSP_004627;
 CC Name=VEGF-2; Synonyms=VEGF120;
 CC IsoID=Q00731-3; Sequence=VSP_004628;
 CC -|- TISSUE SPECIFICITY: In developing embryos, expressed mainly in the
 CC choroid plexus, paraventricular neuroepithelium, placenta and
 CC kidney glomeruli. Also found in bronchial epithelium, adrenal
 CC gland and in seminiferous tubules of testis. High expression of
 CC VEGF continues in glomeruli and choroid plexus in adults.
 CC -|- DOMAIN: VEGF-3 contains a basic insert which acts as a cell
 CC retention signal.
 CC -|- SIMILARITY: Belongs to the PDGF/VEGF growth factor family.

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 or send an email to license@isb-sib.ch).
 CC
 DR EMBL; S37052; AB22252.1;
 DR EMBL; S38083; AB22253.1;
 DR EMBL; S38100; AB22254.1;
 DR EMBL; M95200; AAA40547.1;
 DR EMBL; U41383; -; NOT_ANNOTATED_CDS.
 DR PIR; A44881; A44881.
 DR PIR; B44881; B44881.
 DR HSSP; P15692; 2VPF.
 DR MGI; 103178; Vegfa.
 DR InterPro; IPR000072; PD_growth_factor.

Pfam; PF00341; PDGF; 1.
DR SMART; SM00141; PDGF; 1.
DR PROSITE; PS00249; PDGF-1; 1.
DR Mitogen; Angiogenesis_2; Growth factor; Glycoprotein; Signal;
KW Heparin-binding; Alternative splicing; Multigene family.
FT CHAIN 1 26
 VASCULAR ENDOTHELIAL GROWTH FACTOR A.
 FT CHAIN 27 214
 BY SIMILARITY.
 FT DISULFID 51 93
 BY SIMILARITY.
 FT DISULFID 82 127
 BY SIMILARITY.
 FT DISULFID 86 129
 BY SIMILARITY.
 FT DISULFID 76 76
 INTERCHAIN (BY SIMILARITY).
 FT DISULFID 85 85
 INTERCHAIN (BY SIMILARITY).
 FT CARBONYL 100 100
 N-LINKED (GLCNAC. . .) (PROBABLE).
 FT VARSPLITC 140 140
 K -> N (In isoform VEGF-1).
 FT /FTId=VSP_004626.
 FT VARSPLITC 141 164
 Missing (In isoform VEGF-1).
 FT /FTId=VSP_004627.
 FT VARSPLITC 141 208
 Missing (In isoform VEGF-2).
 FT /FTId=VSP_004628.
 FT CONFLICT 117 118
 GE -> ER (IN REF. 2).
 SQ SEQUENCE 214 AA; 25283 MW; B554051E-BB6E17 CRC64;

Query Match 37.9% Score 320.5; DB 1; Length 214;
 Best Local Similarity 48.1%; Pred. No. 4.1e-26; Indels 1; Gaps 1;
 Matches 62; Conservative 20; Mismatches 46; Sequence-Displayed

Qy 21 SGAGSAGNNSTMEVVNFNEWGRSYCRPMKLVYTADEHNEVSHIFSPSCVLLSRCS 80
 Db 24 SQRAPTTGEQKSHEVIRKFMDVYQRSYCRPCTTLDVFEQYDEIEIYFKPSCVPLMRCA 83

Qy 81 GCGGDEGHCVALKRANTQMQLKKIPPRDHSYVEMTSQDVLCBRPILEBTTRAKRK 140
 Db 94 GGCNDEALECVPTSESNITMQIMRIKPHQSQH-IGEMSFQHSRCRCPKCDRTKPEKKS 142

Qy 141 TKGKRKRSK 149
 Db 143 VEGKGKGK 151

RESULT 7
 ID VEGA_RAT STANDARD; PRT; 214 AA.
 AC P16612; Q9JXK7; Q9QXG6; Q9QXG7;
 DT 01-AUG-1990 (Rel. 15, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Vascular endothelial growth factor A precursor (VEGF-A) (Vascular permeability factor) (VPF).
 GN VEGF OR VEGFA.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 RN RXBLINE-90207249; PubMed=2205795;
 RA Conn G., Bayne M.L., Soderman D.D., Kwok P.W., Sullivan K.A., Palisi T.M., Hope D.A., Thomas K.A.,
 RT "Amino acid and cDNA sequences of a vascular endothelial cell mitogen that is homologous to platelet-derived growth factor.";
 RP proc. Natl. Acad. Sci. U.S.A. 87:2628-2633 (1990).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM VEGF-A164), AND SEQUENCE OF 27-190.
 RX MEDLINE-21092309; PubMed=11163598;
 RA Ishii H., Oota I., Takuma T., Inomata K.;
 RT "Developmental expression of vascular endothelial growth factor in the masticator muscle of rats.";
 RL Arch. Oral Biol. 46:77-82 (2001).
 RN SEQUENCE OF 27-40.

RC TISSUE=Glia tumor;
 RX MEDLINE=95221439; PubMed=7706320; Kwok P.W., Trivedi P.G., Disalvo J., Bayne M.L., Conn G., Thomas K.A.;
 RA Soderman D.D., Palisi T.M., Sullivan K.A., Thomas K.A.;
 RT "Purification and characterization of a naturally occurring vascular endothelial growth factor/placenta growth factor heterodimer.";
 RL J. Biol. Chem. 270:7717-7723 (1995).
 CC -!- FUNCTION: Growth factor active in angiogenesis, vasculogenesis and endothelial cell growth. It induces endothelial cell proliferation, promotes cell migration, inhibits apoptosis, and induces permeabilization of blood vessels. It binds to the VEGFR1/Fit-1 and VEGFR2/Kdr receptors and to heparan sulfate and heparin (By similarity).
 CC -!- SUBUNIT: Homodimer; disulfide-linked. Also found as heterodimer with PIGF (By similarity).
 CC -!- SUBCELLULAR LOCATION: VEGF-A120 is acidic and freely secreted. VEGF-A164 is more basic, has heparin-binding properties and, although a significant proportion remains cell-associated, most is freely secreted. VEGF-A188 is very basic; it is cell-associated after secretion and is bound avidly to heparin and the extracellular matrix, although it may be released as a soluble form by heparin, heparinase or plasmin (By similarity).
 CC -!- ALTERNATIVE PRODUCTS:
 CC -!- ALTERNATIVE splicing; Named isoforms=4;
 CC Comment=Additional isoforms seem to exist;
 Name=VEGF-A188;
 IsoId=P16612-1; Sequence=VSP_004630;
 Name=VEGF-A164;
 IsoId=P16612-2; Sequence=VSP_004629; VSP_004630;
 Name=VEGF-A144;
 IsoId=P16612-3; Sequence=VSP_004632;
 Name=VEGF-A120;
 IsoId=P16612-4; Sequence=VSP_004631;
 CC -!- TISSUE SPECIFICITY: Expressed in the pituitary, in brain, in particular in supraoptic and paraventricular nuclei and the choroid plexus. Also found abundantly in the corpus luteum of the ovary and in kidney glomeruli.
 CC -!- SIMILARITY: Belongs to the PDGF/VEGF growth factor family.
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 DR EMBL; M32167; AAA41211.1; -.
 DR InterPro; IPR000072; PD_growth_factor.
 DR EMBL; AF215726; AAF1911.1; -.
 DR Pfam; PF0141; PDGF; 1.
 DR SMART; SM00141; PDGF; 1.
 DR PROSITE; PS00249; PDGF; 1.
 DR HSSP; P15692; 1YBP.
 DR InterPro; IPR000072; PD_growth_factor.
 DR Ptnam; PFD001629; PD growth_factor; 1.
 DR SMART; SM00141; PDGF; 1.
 DR PROSITE; PS00249; PDGF; 1.
 DR PROSITE; PBS0278; PDGF; 2.1.
 KW Mitogen; Angiogenesis; Growth factor; Glycoprotein; Signal; Heparin-binding; Alternative splicing; Multigene Family.
 FT SIGNAL 1 26
 FT CHAIN 27 214
 FT DISULFID 51 93
 FT DISULFID 82 127
 BY SIMILARITY.
 FT DISULFID 86 129
 BY SIMILARITY.
 FT DISULFID 76 76
 INTERCHAIN (BY SIMILARITY).
 FT DISULFID 85 85
 INTERCHAIN (BY SIMILARITY).
 FT CARBONYL 100 100
 N-LINKED (GLCNAC. . .).
 FT VARSPLIC 140 140
 K -> N (In isoform VEGF-A164).
 /FTId=VSP_004629.
 Missing (In isoform VEGF-A164).
 /FTId=VSP_004630.
 Missing (In isoform VEGF-A120).
 /FTId=VSP_004631.
 Missing (In isoform VEGF-A188).
 /FTId=VSP_004632.
 Missing (In isoform VEGF-A144).

				"AIDS-associated Kaposi's sarcoma cells in culture express vascular endothelial growth factor." [6]
RT	VARSPLIC	1.65	208	Missing (In VSP 004631).
FT	CONFLICT	1.01	101	/FTid=VSP 004632.
FT	SEQUENCE	21.4 AA;	25239 MW;	V->A (IN REF. 2; AAF19212).
SQ	Query	Match	37.8% ; Score 319.5 ; DB 1 ; Length 214 ;	
SQ	Query	Best Local Similarity	48.1% ; Pred. No. 5.2e-26 ; Mismatches 20 ; Indels 1 ; Gaps 1 ; Matches 62 ; Conservative 20 ; N mismatches 46 ; CRC64 ;	
Db	Qy	21	SGAAGSAGNNTMEVPPNEWGRSYCRPPIETLVDIFEPYDIEYFKPSCLTSLRSQS 80	
Db	Qy	24	SQAPPTTEQEKAEEVKMDVYKSYCRPPIETLVDIFEPYDIEYFKPSCLTLMRCA 83	
Db	Qy	81	GCCCGDEGLHCVALKTANITMQLIKPNNPRDPHSYVEMTFSQDVLCRPLLETTKAERK 140	
Ddb	B4	Q9TH58 ; Q9UL23 ;	B4 GCCNDEALECVPSTSNSNVTMQIMRIKPHOSQH-1GEMSLFLQHSRCECREPKDRTPKPKRS 142	
Db	Qy	141	TGGRKQSK 149	
Db	Qy	143	VRGKGKQK 151	
				RESULT 8
		VEGA_HUMAN		
		VEGA_ID	STANDARD; PRT; 232 AA.	
		AC	P16592 ; O60720 ; O75875 ; Q16889 ; Q96LB2 ; Q9NW5 ; Q9H1W9 ;	
		AC	Q9TH58 ; Q9UL23 ;	
		DT	01-APR-1990 (Rel. 1.4, Created)	
		DT	28-FEB-2003 (Rel. 41, Last sequence update)	
		DT	15-MAR-2004 (Rel. 43, Last annotation update)	
			Vascular endothelial growth factor A precursor (VEGFA) (vascular permeability factor) (VPF).	
			VEGF or VEGFA.	
			Homo sapiens (Human).	
			Bulmaryoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
		NCBI_TaxID	=9606 ;	
		OC		
		OX		
		SEQUENCE	FROM N.A. (ISOFORMS VEGF189 AND VEGF165).	
		RR	MEDLINE=9006908 ; PubMed=247986 ;	
		RX	Leng D.W., Cachianes G., Kuang W.-J., Goeddel D.V., Ferrara N. ;	
		RT	"Vascular endothelial growth factor is a secreted angiogenic mitogen." ;	
		RT	Science 246:1306-1309 (1989).	
		RT		
		RN	SEQUENCE FROM N.A. (ISOFORM VEGF189), AND PARTIAL SEQUENCE.	
		RX	MEDLINE=9006909 ; PubMed=247987 ;	
		RA	Keck P.J., Hauser S.D., Krivi G., Sanzo K., Warren T., Feder J., Connolly D.T. ;	
		RT	"Vascular permeability factor, an endothelial cell mitogen related to PDGF." ;	
		RT	Science 246:1309-1312 (1989).	
		RL		
		RR	SEQUENCE FROM N.A. (ISOFORM VEGF189).	
		RX	MEDLINE=1268012 ; PubMed=1711045 ;	
		TX	Tischer B., Mitchell R., Hartman T., Silva M., Gospodarowicz D. , Fiddes J.C., Abraham J.A. ;	
		RA	"The human gene for vascular endothelial growth factor. Multiple protein forms are encoded through alternative exon splicing." ;	
		RT	J. Biol. Chem. 266:11947-11954 (1991).	
		RT		
		RN	SEQUENCE FROM N.A. (ISOFORM VEGF206).	
		RX	MEDLINE=9216B017 ; PubMed=1791881 ;	
		TX	Houck V., Ferrara N., Winer J., Cachianes G., Li B., Leung D.W. ; Connolly D.T. ;	
		RA	"The vascular endothelial growth factor family: identification of a fourth molecular species and characterization of alternative splicing of RNA." ;	
		RT	Endocrinol. 5:1806-1814 (1991).	
		RT		
		RN	SEQUENCE OF N.A. (ISOFORM VEGF165).	
		RX	MEDLINE=32231979 ; PubMed=1567395 ;	
		RA	Weindel K., Marne D., Weich H.A. ;	
		RP	Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.	
		RN	SEQUENCE OF N.A. (ISOFORM VEGF183).	
		RX	MEDLINE=114-209 FROM N.A. (ISOFORM VEGF183).	

TISSUE=Retina;
 RX MEDLINE=99165303; PubMed=10067980;
 RA Jingjing L., Xue Y., Agarwal N., Roque R.S./
 RT "Human Muller cells express VEGF183, a novel spliced variant of
 vascular endothelial growth factor.",
 Invest. Ophthalmol. Vis. Sci. 40:752-759 (1999).
 [17]

PRELIMINARY SEQUENCE OF 27-36; 43-50 AND 59-81.
 MEDLINE=9006112; PubMed=284205;
 RX Connolly D.T., Olander J.V., Heuvelman D., Nelson R., Morsell R.,
 RA Siegel N., Haymore B.L., Leimgruber R., Feder J.;
 RT "Human vascular permeability factor. Isolation from U937 cells.";
 RL Eur. J. Biol. Chem. 264:20017-20024 (1989).
 BN [18]

SEQUENCE OF 27-41.
 MEDLINE=9315946; PubMed=7678805;
 RA Fiebich B.L., Jaeger B., Schoellmann C., Weindel K., Wilting J.,
 RA Kochs G., Marne D., Hug H., Weich H.A.;
 RT "Synthesis and assembly of functionally active human vascular
 endothelial growth factor homodimers in insect cells.,";
 RL Eur. J. Biochem. 211:19-26 (1993).
 RN [19]

RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 34-135.
 RX MEDLINE=97352774; PubMed=92070677;
 RA Muller Y.A., Li B., Christinger H.W., Wells J.A., Cunningham B.C.,
 RA de Vos A.M.;
 RT "Vascular endothelial growth factor: crystal structure and functional
 mapping of the kinase domain receptor binding site.,";
 RL Proc. Natl. Acad. Sci. U.S.A. 94:7192-7197 (1997).
 [20]

RN X-RAY CRYSTALLOGRAPHY (1.93 ANGSTROMS) OF 34-135.
 RX MEDLINE=98035455; PubMed=92151807;
 RA Muller Y.A., Christinger H.W., Keyt B.A., de Vos A.M.;
 RT refined to 1.93-A resolution: multiple copy flexibility and receptor
 binding.,";
 RL Structure 5:1325-1338 (1997).
 RN [21]

RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF 39-134.
 RX MEDLINE=99119204; PubMed=922112;
 RA Wiesmann C., Christinger H.W., Cochran A.G., Cunningham B.C.,
 RA Fairbrother W.J., Keenan C.J., Meng G., de Vos A.M.;
 RT "Crystal structure of the complex between VEGF and a receptor-blocking
 peptide.,";
 RL Biochemistry 37:17765-17772 (1998).
 RN [22]

RP STRUCTURE BY NMR OF 34-135.
 RX MEDLINE=97477915; PubMed=3136848;
 RA Starovsnik M.A.;
 RT "1H, 13C, and 15N backbone assignment and secondary structure of the
 receptor-binding domain of vascular endothelial growth factor.,";
 RL Protein Sci. 6:2250-2260 (1997).
 RN [23]

RP STRUCTURE BY NMR OF 137-215.
 RX MEDLINE=9828440; PubMed=9334701;
 RA Starovsnik M.A., Champé M.A., Christinger H.W., Keyt B.A.,
 RA Fairbrother W.J., Champé M.A., Christinger H.W., Keyt B.A.,
 RT "Solution structure of the heparin-binding domain of vascular
 endothelial growth factor.,";
 RL Structure 6:637-648 (1998).
 RN [24]

RP FUNCTION.
 RX MEDLINE=21320504; PubMed=11427521;
 RA Murphy J.F., Fitzgerald D.T.;
 RT "Vascular endothelial growth factor induces cyclooxygenase-dependent
 proliferation of endothelial cells via the VEGF-2 receptor.";
 RL PASEB J. 15:1667-1669 (2001).
 CC - FUNCTION: Growth factor active in angiogenesis, vasculogenesis and
 CC endothelial cell growth. It induces endothelial cell
 CC proliferation, promotes cell migration, inhibits apoptosis, and
 CC induces permeabilization of blood vessels. It binds to the
 VEGFR1/Fit-1 and VEGFR2/Kdr receptors and to heparan sulfate and
 CC heparin (By similarity).
 CC - SUBUNIT: Homodimer; disulfide-linked. Also found as heterodimer
 CC with PIGF (By similarity).
 CC - SUBCELLULAR LOCATION: Secreted but remains associated to cells or
 CC to the extracellular matrix unless released by heparin (By
 CC similarity).
 CC - SIMILARITY: Belongs to the PDGF/VEGF growth factor family.

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CC EMBL; AB053350; BAB20890_1; -.

CC HSSP; P15692; 1VGH.

CC DR InterPro; IPR00400; GF_cysknot.

CC DR InterPro; IPR00072; PD_growth_factor.

CC DR Pfam; PF0141; PDGF_1.

CC DR PRINTS; PRO043B; GF_CYSKNOT.

CC DR ProDom; PD001629; PD_growth_factor_1.

CC DR SMART; SM00141; PDGF_1.

CC DR PROSITE; PS00249; PDGF_1.

CC DR PROSITE; PS50278; PDGF_2.

CC DR Mitogen; Angiogenesis_Growth_factor; Glycoprotein_Signal;

CC DR Multigene Family.

CC DR SIGNAL 1 26 POTENTIAL.

CC DR CHAIN 27 190 VASCULAR ENDOTHELIAL GROWTH FACTOR A.

CC DR DISULFID 51 93 BY SIMILARITY.

CC DR DISULFID 82 127 BY SIMILARITY.

CC DR DISULFID 86 129 BY SIMILARITY.

CC DR DISULFID 76 76 INTERCHAIN (BY SIMILARITY).

CC DR CARBOHYD 100 100 N-LINKED (GLCNAC. . .) (POTENTIAL).

CC DR CONFLICT 102 102 T->A (IN REF. 2).

CC DR SEQUENCE 190 AA; 22368 MW; 04DA08D7913047F CRC64;

Query Match 35.0% Score 296 5; DB 1; Length 190;

Best Local Similarity 48.4%; Pred. No. 1..1e-23;

Matches 62; Conservative 17; Mismatches 40; Indels 9; Gaps 2;

Qy 21 SQGAGNSTMEEVVPNNWGRSYCRPEKLVIADEPDNEUSHFSSCSCLLSRCS 80

Db 24 SQAAPMAEGQKPKHEVVKEMDVYQRSCYPETLVIQFQETPDELEYIFKSCVPLMRCG 83

Qy 81 GCGCDEGLHVALKTANITMQLKIPPNRDPHSYVMTFSQDVLCRPILETTK---- 135

Ddb 84 GCNDDEGLECVPTEEFNITMQLMTRPHQGH-IGEMSFLQHNLCKTCPKFDRARQENPC 142

Qy 136 --AERRK 140

Ddb 143 GPCSERRK 150

RESULT 10

VEGA_HORSE VEGA_HORSE STANDARD; PRT; 190 AA.

AC Q9GRK0; ID 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DB Vascular endothelial growth factor A precursor (VEGF-A) (vascular permeability factor) (VPF).

GN Equis caballus (Horse).

OS Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi; OC Equidae; Equidae; Equidae; Equus.

NCBI_TAXID=9796;

RN SEQUENCE FROM N.A.

RA Miura N., Misumi K., Kawahara K., Nakashima M., Fukumitsu S., Kawabata H., Uto N., Oka T., Maruyama T., Sakamoto H., RT "Cloning of cDNA and high-level expression of equine vascular endothelial growth factor (VEGF)"

RT Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.

CC -- FUNCTION: Growth factor active in angiogenesis, and endothelial cell growth. Induces endothelial proliferation and vascular permeability (By similarity).

CC SUBUNIT: Homodimer; disulfide-linked. Also found as heterodimer with PIGF (By similarity).

CC - SUBCELLULAR LOCATION: Secreted but remains associated to cells or to the extracellular matrix unless released by heparin (By similarity).

CC - SIMILARITY: Belongs to the PDGF/VEGF growth factor family.

DR EMBL; AB053350; BAB20890_1; -.

DR HSSP; P15692; 1VGH.

DR InterPro; IPR00400; GF_cysknot.

DR InterPro; IPR00072; PD_growth_factor.

DR Pfam; PF0141; PDGF_1.

DR PRINTS; PRO043B; GF_CYSKNOT.

DR ProDom; PD001629; PD_growth_factor_1.

DR SMART; SM00141; PDGF_1.

DR PROSITE; PS00249; PDGF_1.

DR PROSITE; PS50278; PDGF_2.

DR Mitogen; Angiogenesis_Growth_factor; Glycoprotein_Signal;

DR Multigene Family.

DR SIGNAL 1 26 POTENTIAL.

DR CHAIN 27 190 VASCULAR ENDOTHELIAL GROWTH FACTOR A.

DR DISULFID 51 93 BY SIMILARITY.

DR DISULFID 82 127 BY SIMILARITY.

DR DISULFID 86 129 BY SIMILARITY.

DR DISULFID 76 76 INTERCHAIN (BY SIMILARITY).

DR DISULFID 85 85 INTERCHAIN (BY SIMILARITY).

DR CARBOHYD 100 100 N-LINKED (GLCNAC. . .) (POTENTIAL).

DR SEQUENCE 190 AA; 22312 MW; 87E9E161439E5FB7 CRC64;

Query Match 34.8% Score 294.5; DB 1; Length 190;

Best Local Similarity 48.4%; Pred. No. 1..8e-23;

Matches 62; Conservative 15; Mismatches 42; Indels 9; Gaps 2;

Qy 21 SQGAGNSTMEEVVPNNWGRSYCRPEKLVIADEPDNEUSHFSSCSCLLSRCS 80

Db 24 SQAAPMAEGQKPKHEVVKEMDVYQRSCYPETLVIQFQETPDELEYIFKSCVPLMRCG 83

Qy 81 GCGCDEGLHVALKTANITMQLKIPPNRDPHSYVMTFSQDVLCRPILETTK---- 135

Db 84 GCNDDEGLECVPTEEFNITMQLMTRPHQGH-IGEMSFLQHNLCKTCPKFDRARQENPC 142

Qy 136 --AERRK 140

Db 143 GPCSERRK 150

RESULT 11

VEGA_CHICK STANDARD; PRT; 216 AA.

AC P52582; Q91420; ID 01-OCT-1996 (Rel. 34, Created)

DT 15-JUL-1998 (Rel. 36, Last sequence update)

DB 10-OCT-2003 (Rel. 42, Last annotation update)

DE Vascular endothelial growth factor A precursor (VEGF-A) (vascular permeability factor) (VPF).

GN VEGF OR VEGFA.

OS Gallus gallus (Chicken), and Corvinix coturnix japonica (Japanese quail).

OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Gallinae; OC Gallus.

NCBI_TAXID=9031; RN SEQUENCE FROM N.A.

RC SPECIES=Chicken; TISSUE=Heart; RC SPECIES=Japanese quail; TISSUE=Heart; RC SPECIES=Corvinix coturnix japonica; TISSUE=Heart; RC SPECIES=Takahashi T.;

RT "Chick embryonic ventricular myocytes VEGF";

RT Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.

[2]

RN SEQUENCE FROM N.A. (ISOFORMS VEGF-190; VEGF-166 AND VEGF-146).

RP SPECIES=C. jacchii; TISSUE=Embryo; RC SPECIES=C. jacchii; PubMed=755623;

RX MEDLINE=16005007; PubMed=755623;

RX

Flamme I., von Reutern M., Drexler H.C., Syed-Ali S., Risseau W.;
 RT "Overexpression of vascular endothelial growth factor in the avian embryo induces hypervascularization and increased vascular permeability without alterations of embryonic pattern formation.";
 RL Dev. Biol. 171:395-414 (1995).
 [3]
 RN SEQUENCE OF 60-187 FROM N.A. (ISOFORMS VEGF-190 AND VEGF-166).
 SPECIES=C. c. japonica;
 MEDLINE=95301109; PubMed=7781909;
 RA Flamme I., Breier G., Risseau W.;
 RT "Vascular endothelial growth factor (VEGF) and VEGF receptor 2 (flk-1) are expressed during vasculogenesis and vascular differentiation in the quail embryo.";
 RL Dev. Biol. 169:699-712 (1995).
 -!- FUNCTION: Growth factor active in angiogenesis, vasculogenesis and endothelial cell growth. It induces endothelial cell proliferation, promotes cell migration, inhibits apoptosis, and induces permeabilization of blood vessels. It binds to the VEGFR1/Fit-1 and VEGFR2/Kdr receptors and to heparan sulfate and heparin (By similarity).
 -!- SUBUNIT: Homodimer; disulfide-linked. Also found as heterodimer with PIGF (By similarity).
 CC Event=Alternative splicing; Named isoforms seem to exist;
 CC Comment=Additional isoforms seem to exist;
 CC Name=VEGF-190;
 CC IsoID=P52562-1; Sequence=Displayed;
 CC Name=VEGF-166;
 CC IsoID=P52562-2; Sequence=VSP 004633; VSP 004634;
 CC Note=Has been shown to exist only in quail so far;
 CC Name=VEGF-146;
 CC IsoID=P52562-3; Sequence=vSP 004635; vSP 004636;
 CC Note=Has been shown to exist only in quail so far;
 CC -!- TISSUE SPECIFICITY: Abundantly and equally expressed in heart and liver. In kidney glomeruli, brain and yolk sac, VEGF-166 is 5- to 10-times more abundant than VEGF-190.
 CC -!- DEVELOPMENTAL STAGE: VEGF-166 is expressed early at day 1 and is upgraded during gastrulation. Expression of VEGF-190 is detectable only from day 2.
 CC -!- DOMAIN: VEGF-190 contains a basic insert which acts as a cell retention signal.
 CC -!- SIMILARITY: Belongs to the PDGF/VEGF growth factor family.

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CC DR EMBL; S79680; AAB35371.1; -.
 DR HSSP; P15632; IVGK.
 DR InterPro: IPR000072; PD_growth_factor.
 PFam: PF00341; PDGF; 1.
 ProDom: PD001629; PD growth_factor; 1.
 SMART: SM00141; PDGF; 1.
 DR PROSITE: PS00249; PDGF; 1.
 DR PSSM: PS50278; PDGF; 2; 1.
 KW Mitogen; Angiogenesis; Growth factor; Glycoprotein; Signal;
 KW Heparin-binding; Alternative splicing; Multigene family.
 SIGNAL 1 26
 CHAIN 27 216
 FT DISULFID 52 94
 BY SIMILARITY.
 FT DISULFID 83 128
 BY SIMILARITY.
 FT DISULFID 87 130
 BY SIMILARITY.
 FT DISULFID 77 77
 INTERCHAIN (BY SIMILARITY).
 FT DISULFID 86 86
 INTERCHAIN (BY SIMILARITY).
 FT CARBOHYD 101 101
 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT VARSPLIC 142 142
 K->N (in isoform VEGF-166).
 /FTId=VSP 004633.
 FT VARSPLIC 143 166
 Missing (in isoform VEGF-166).

/FTId=VSP 004634.
 F -> L (in isoform VEGF-146).
 /FTId=VSP 004635.
 Missing (In isoform VEGF-146).
 RL Dev. Biol. 171:395-414 (1995).
 [3]
 RN SEQUENCE 216 AA; 25203 MW; 82E669C2F6FDA7 CRC64;
 SQ Query Match 34.5%; Score 291.5; DB 1; Length 216;
 Best Local Similarity 42.3%; Pred. No. 4.3e-23;
 Matches 60; Conservative 29; Mismatches 46; Indels 7; Gaps 3;
 Qy 21 SQGALSAGNNST-MEVVPFNEVWGRSYCRPMKLYYTADEHPNEVSHIFSPSCVLLSRC 79
 DB 24 SKAPALDGERRKPNENVTKFLEYERSFCRTIELVLFQEDEVETFRPSCVPLMRC 83
 Qy 80 SGCGDDEGLHCTVALKTANITMQILKIPNDRDHSYVEMTFSQDVLCRPILET----T 134
 DB 84 AGCGDDELECYFDVNVNTMIRAKPHQSOH-TAEMSFLQHSKCDCRPKDVKNKQEK 142
 Qy 135 KAERKRKGKQRKOSKTKPQEFP 156
 DB 143 KSKRGKRGKGQKRKRGKRGKRYKPP 164
 RESULT 12
 VEGA_BOVIN STANDARD; PRT; 190 AA.
 ID VEGA_BOVIN
 AC P15691;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Vascular endothelial growth factor A precursor (VEGFR-A) (Vascular permeability factor) (VPF).
 DE VEGF or VEGFA.
 GN Bos tauri (Bovine).
 OS Bovidae; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bivalvia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.
 OC NCB Taxid:9913;
 RN [1] RP SEQUENCE FROM N.A. AND SEQUENCE OF 27-47.
 RX MBIDLINE=90069608; PubMed=479386;
 RA Leung D.W., Cachianes G., Kuang W.-J., Goeddel D.V., Ferrara N.;
 RT "Vascular endothelial growth factor is a secreted angiogenic mitogen.";
 RT Science 246:1306-1309 (1989).
 RN [2] RP SEQUENCE OF 27-190 FROM N.A. (ISOFORMS ALPHA AND BETA).
 RX MBIDLINE=90121225; PubMed=2610687;
 RA Tischer E., Gospodarowicz D., Mitchell R., Silva M., Schilling J., Lau K., Crisp T., Piddes J.C., Abraham J.A.;
 RA RT "Vascular endothelial growth factor; a new member of the platelet-derived growth factor gene family";
 RL Biochem. Biophys. Res. Commun. 165:1198-1206 (1989).
 RN [3] RP SEQUENCE OF 27-31.
 RX MEDLINE=89265586; PubMed=2735925;
 RA Ferrara N., Henzel W.J.;
 RT "Pituitary follicular cells secrete a novel heparin-binding growth factor specific for vascular endothelial cells.";
 RT Biochem. Biophys. Res. Commun. 161:851-858 (1989).
 CC -!- FUNCTION: Growth factor active in angiogenesis, vasculogenesis and endothelial cell growth. It induces endothelial cell proliferation, promotes cell migration, inhibits apoptosis, and induces permeabilization of blood vessels. It binds to the VEGFR1/Fit-1 and VEGFR2/Kdr receptors and to heparan sulfate and heparin (By similarity).
 CC -!- SUBUNIT: Homodimer; disulfide-linked. Also found as heterodimer with PIGF (By similarity).
 CC -!- SUBCELLULAR LOCATION: Secreted but remains associated to cells or to the extracellular matrix unless released by heparin (By similarity).
 CC -!- ALTERNATIVE PRODUCTS:

Event=Alternative splicing; Named isoforms=2;	
Name=Alpha;	
IsoId=15691-1; Sequence=Displayed;	
IsoId=15691-2; Sequence=VSP_004613, VSP_004614; Belongs to the PDGF/VEGF growth factor family.	
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EMBL: M32976; AAAJ0502.1; -.	
EMBL: M31836; AAAJ0804.1; -.	
PTR: A33787; A33787.	
PIR: B40080; B40080.	
HSSP: P15692; LVGH.	
InterPro: IPR002400; GF_cysknat.	
InterPro: IPR000722; PD_growth_factor.	
PRINTS: PF00341; PDGF_1.	
PRODOM: PD001629; PDGFSKNOT.	
SMART: SMM00141; PDGF_1.	
PROSITE: PS00249; PDGF_1.	
PROSITE: PS50278; PDGF_2.	
Mitogen; Angiogenesis; Growth factor; Glycoprotein; Signal; Heparin-binding; Alternative splicing; Multigene family.	
SIGNAL: 1 26	
CHAIN: 27 190 VASCULAR ENDOTHELIAL GROWTH FACTOR A.	
DISULFID: 51 93	
DISULFID: 82 127	
DISULFID: 86 129	
DISULFID: 76 76 INTERCHAIN (BY SIMILARITY).	
DISULFID: 85 85 INTERCHAIN (BY SIMILARITY).	
CARBOHYD: 100 100 N-Missing (in isoform Beta).	
VARSPLIC: 139 183 Missing (in isoform Beta). /F1d4VSP_004613.	
VARSPLIC: 184 R -> K (in isoform Beta).	
SEQUENCE: 190 AA; 22310 MW; /FTid=VSP_004614; EDBF903E46E24789 CRC64;	
Query Match 33.5%; Score 283.5; DB 1; Length 190; Best Local Similarity 46.9%; Pred. No. 2.5e-22; Matches 60; Conservative 16; Mismatches 43; Indels 9; Gaps 2;	
Y 21 SQGALSAGNNTSEMEVPFNEVGRSYCRPEMKLVIADEHPNEYSHIFPSCLVLSRCS 80	
b 24 SQAAPMAGEGQKPHVKEFYMDVYQSFRECPTEFLVDIFQYPDELEFIFPSCLVLMRCG 83	
Y 81 GCGGDEGLHCVALKTANITMQLKPPNRPHSYMTFSQDVLCBRCPLLETTK-----135	
b 84 GCCNDESLEYCPTEEFNITMQLIMRXPHQSOH-IGEMSFLOHNKCECRPKDKARQENPC 142	
Y 136 --AERRK 140	
b 143 GPCSERRK 150	
Q99PS1; D_VEGA_MESAU STANDARD; PRT; 190 AA.	
RESULT 13	
TEGAA_MESAU	
Q99PS1; C	
Y 21 SGQLSAGNNNTSEMEVPFNEVGRSYCRPEMKLVIADEHPNEYSHIFPSCLVLSRCS 80	
b 24 SQAAPPTEGEOKAHGUVFMDVYRSYCHPILETVDIFQYPDELEFIFPSCLVLMRCG 83	
Qy 81 GCCGDBGLHCVALKTANITMQLKPPNRPHSYMTFSQDVLCBRCPLLETTK-----135	
Db 84 GCCSDDALECYPTSEEINTQIMRXPHQSOH-IGEMSFLOHNKCECRPKDKARQENHC 142	
Qy 136 --AERRK 140	
Db 143 EPCSERRK 150	
Event=Alternative splicing; Named isoforms=2;	
Name=Beta;	
IsoId=15691-1; Sequence=Displayed;	
IsoId=15691-2; Sequence=VSP_004613, VSP_004614; Belongs to the PDGF/VEGF growth factor family.	
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EMBL: M32976; AAAJ0502.1; -.	
EMBL: M31836; AAAJ0804.1; -.	
PTR: A33787; A33787.	
PIR: B40080; B40080.	
HSSP: P15692; LVGH.	
InterPro: IPR002400; GF_cysknat.	
InterPro: IPR000722; PD_growth_factor.	
PRINTS: PF00341; PDGF_1.	
PRODOM: PD001629; PDGFSKNOT.	
SMART: SMM00141; PDGF_1.	
PROSITE: PS00249; PDGF_1.	
PROSITE: PS50278; PDGF_2.	
Mitogen; Angiogenesis; Growth factor; Glycoprotein; Signal; Heparin-binding; Alternative splicing; Multigene family.	
SIGNAL: 1 26	
CHAIN: 27 190 VASCULAR ENDOTHELIAL GROWTH FACTOR A.	
DISULFID: 51 93	
DISULFID: 82 127	
DISULFID: 86 129	
DISULFID: 76 76 INTERCHAIN (BY SIMILARITY).	
DISULFID: 85 85 INTERCHAIN (BY SIMILARITY).	
CARBOHYD: 100 100 N-Missing (in isoform Beta).	
VARSPLIC: 139 183 Missing (in isoform Beta). /F1d4VSP_004613.	
VARSPLIC: 184 R -> K (in isoform Beta).	
SEQUENCE: 190 AA; 22310 MW; /FTid=VSP_004614; EDBF903E46E24789 CRC64;	
Query Match 33.4%; Score 282.5; DB 1; Length 190; Best Local Similarity 46.1%; Pred. No. 3.2e-22; Matches 59; Conservative 16; Mismatches 44; Indels 9; Gaps 2;	
Qy 21 SGQLSAGNNNTSEMEVPFNEVGRSYCRPEMKLVIADEHPNEYSHIFPSCLVLSRCS 80	
Db 24 SQAAPPTEGEOKAHGUVFMDVYRSYCHPILETVDIFQYPDELEFIFPSCLVLMRCG 83	
Qy 81 GCCGDBGLHCVALKTANITMQLKPPNRPHSYMTFSQDVLCBRCPLLETTK-----135	
Db 84 GCCSDDALECYPTSEEINTQIMRXPHQSOH-IGEMSFLOHNKCECRPKDKARQENHC 142	
Event=Alternative splicing; Named isoforms=2;	
Name=Alpha;	
IsoId=15691-1; Sequence=Displayed;	
IsoId=15691-2; Sequence=VSP_004613, VSP_004614; Belongs to the PDGF/VEGF growth factor family.	
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PRODOM: PD001629; PDGFSKNOT.	
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PROSITE: PS00249; PDGF_1.	
PROSITE: PS50278; PDGF_2.	
Mitogen; Angiogenesis; Growth factor; Glycoprotein; Signal; Heparin-binding; Multigene family.	
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SEQUENCE: 190 AA; 22310 MW; /FTid=VSP_004614; EDBF903E46E24789 CRC64;	
Query Match 33.4%; Score 282.5; DB 1; Length 190; Best Local Similarity 46.1%; Pred. No. 3.2e-22; Matches 59; Conservative 16; Mismatches 44; Indels 9; Gaps 2;	
Qy 21 SGQLSAGNNNTSEMEVPFNEVGRSYCRPEMKLVIADEHPNEYSHIFPSCLVLSRCS 80	
Db 24 SQAAPPTEGEOKAHGUVFMDVYRSYCHPILETVDIFQYPDELEFIFPSCLVLMRCG 83	
Qy 81 GCCGDBGLHCVALKTANITMQLKPPNRPHSYMTFSQDVLCBRCPLLETTK-----135	
Db 84 GCCSDDALECYPTSEEINTQIMRXPHQSOH-IGEMSFLOHNKCECRPKDKARQENHC 142	
Event=Alternative splicing; Named isoforms=2;	
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IsoId=15691-2; Sequence=VSP_004613, VSP_004614; Belongs to the PDGF/VEGF growth factor family.	
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PROSITE: PS00249; PDGF_1.	
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Query Match 33.4%; Score 282.5; DB 1; Length 190; Best Local Similarity 46.1%; Pred. No. 3.2e-22; Matches 59; Conservative 16; Mismatches 44; Indels 9; Gaps 2;	
Qy 21 SGQLSAGNNNTSEMEVPFNEVGRSYCRPEMKLVIADEHPNEYSHIFPSCLVLSRCS 80	
Db 24 SQAAPPTEGEOKAHGUVFMDVYRSYCHPILETVDIFQYPDELEFIFPSCLVLMRCG 83	
Qy 81 GCCGDBGLHCVALKTANITMQLKPPNRPHSYMTFSQDVLCBRCPLLETTK-----135	
Db 84 GCCSDDALECYPTSEEINTQIMRXPHQSOH-IGEMSFLOHNKCECRPKDKARQENHC 142	
Event=Alternative splicing; Named isoforms=2;	
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IsoId=15691-2; Sequence=VSP_004613, VSP_004614; Belongs to the PDGF/VEGF growth factor family.	
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InterPro: IPR000722; PD_growth_factor.	
PRINTS: PF00341; PDGF_1.	
PRODOM: PD001629; PDGFSKNOT.	
SMART: SMM00141; PDGF_1.	
PROSITE: PS00249; PDGF_1.	
PROSITE: PS50278; PDGF_2.	
Mitogen; Angiogenesis; Growth factor; Glycoprotein; Signal; Heparin-binding; Multigene family.	
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Query Match 33.4%; Score 282.5; DB 1; Length 190; Best Local Similarity 46.1%; Pred. No. 3.2e-22; Matches 59; Conservative 16; Mismatches 44; Indels 9; Gaps 2;	
Qy 21 SGQLSAGNNNTSEMEVPFNEVGRSYCRPEMKLVIADEHPNEYSHIFPSCLVLSRCS 80	
Db 24 SQAAPPTEGEOKAHGUVFMDVYRSYCHPILETVDIFQYPDELEFIFPSCLVLMRCG 83	
Qy 81 GCCGDBGLHCVALKTANITMQLKPPNRPHSYMTFSQDVLCBRCPLLETTK-----135	
Db 84 GCCSDDALECYPTSEEINTQIMRXPHQSOH-IGEMSFLOHNKCECRPKDKARQENHC 142	
Event=Alternative splicing; Named isoforms=2;	
Name=Beta;	
IsoId=15691-1; Sequence=Displayed;	
IsoId=15691-2; Sequence=VSP_004613, VSP_004614; Belongs to the PDGF/VEGF growth factor family.	
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EMBL: M31836; AAAJ0804.1; -.	
PTR: A33787; A33787.	
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HSSP: P15692; LVGH.	
InterPro: IPR002400; GF_cysknat.	
InterPro: IPR000722; PD_growth_factor.	
PRINTS: PF00341; PDGF_1.	
PRODOM: PD001629; PDGFSKNOT.	
SMART: SMM00141; PDGF_1.	
PROSITE: PS00249; PDGF_1.	
PROSITE: PS50278; PDGF_2.	
Mitogen; Angiogenesis; Growth factor; Glycoprotein; Signal; Heparin-binding; Multigene family.	
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CHAIN: 27 190 VASCULAR ENDOTHELIAL GROWTH FACTOR A.	
DISULFID: 51 93	
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DISULFID: 76 76 INTERCHAIN (BY SIMILARITY).	
DISULFID: 85 85 INTERCHAIN (BY SIMILARITY).	
CARBOHYD: 100 100 N-Missing (in isoform Beta).	
VARSPLIC: 139 183 Missing (in isoform Beta). /F1d4VSP_004613.	
VARSPLIC: 184 R -> K (in isoform Beta).	
SEQUENCE: 190 AA; 22310 MW; /FTid=VSP_004614; EDBF903E46E24789 CRC64;	
Query Match 33.4%; Score 282.5; DB 1; Length 190; Best Local Similarity 46.1%; Pred. No. 3.2e-22; Matches 59; Conservative 16; Mismatches 44; Indels 9; Gaps 2;	
Qy 21 SGQLSAGNNNTSEMEVPFNEVGRSYCRPEMKLVIADEHPNEYSHIFPSCLVLSRCS 80	
Db 24 SQAAPPTEGEOKAHGUVFMDVYRSYCHPILETVDIFQYPDELEFIFPSCLVLMRCG 83	
Qy 81 GCCGDBGLHCVALKTANITMQLKPPNRPHSYMTFSQDVLCBRCPLLETTK-----135	
Db 84 GCCSDDALECYPTSEEINTQIMRXPHQSOH-IGEMSFLOHNKCECRPKDKARQENHC 142	

RESULT 14 VEGA_SHEEP ID_VEGA_SHEEP AC_P50412; DT_01-OCT-1996 (Rel. 34, Created) DT_01-OCT-1996 (Rel. 34, Last sequence update) DT_10-OCT-2003 (Rel. 42, Last annotation update) DE_vascular endothelial growth factor A precursor (VEGF-A) (vascular permeability factor) (VPF). GN_VEGF OR VEGFA. OS_Ovis aries (Sheep). OC_Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC_Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; OC_NCBITAXID=9940; RN_RPSEQUENCE FROM N.A. RC_TISSUE-Kidney; RX_MEDLINE#97117958; PubMed=8958842; RA_Redmer D.A.; Dai Y.; Li J.; Charnock-Jones D.S.; Smith S.K., RA_Reynolds L.P.; Moor R.M.; RT_Characterization and expression of vascular endothelial growth factor (VEGF) in the ovine corpus luteum.; RL_J. Reprod. Fertil. 108:157-165(1996); CC_FUNCION: Growth factor active in angiogenesis, vasculogenesis and endothelial cell growth. It induces endothelial cell proliferation, promotes cell migration, inhibits apoptosis, and induces permeabilization of blood vessels. It binds to the VEGFR1/Flt-1 and VEGFR2/Kdr receptors and to heparan sulfate and heparin (By similarity). CC_SUBUNIT: Homodimer; disulfide-linked. Also found as heterodimer with PIGF (By similarity). CC_SIMILARITY: Belongs to the PDGF/VEGF growth factor family. CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch). CC DR_PIR; S57956; S57196; -. CC DR_HSSP; P15652; 1VPP. CC DR_InterPro; IPR00410; GP_cysknot. CC DR_Pfam; PF00341; PDGF; 1. CC DR_PRINTS; PR00038; GFCKYSKNOT. CC DR_ProDom; PD001622; PD_growth_factor; 1. CC DR_SM00141; PDGF; 1. CC DR_PROSITE; PS00249; PDGF; 1. CC DR_PROSITE; PS00278; PDGF; 2; 1. CC KW_Mitogen; Angiogenesis; Growth factor; Glycoprotein; Signal; Heparin-binding; Multigene family. CC FT_SIGNAL 1 26 BY SIMILARITY. CC FT_CHAIN 27 146 BY SIMILARITY. CC FT_DISULFID 51 93 BY SIMILARITY. CC FT_DISULFID 82 127 BY SIMILARITY. CC FT_DISULFID 86 129 BY SIMILARITY. CC FT_DISULFID 76 76 INTERCHAIN (BY SIMILARITY). CC FT_DISULFID 85 85 INTERCHAIN (BY SIMILARITY). CC FT_CARBONYD 100 100 N-LINKED (GLCNAC. . .) (POTENTIAL). CC SQ_SEQUENCE 146 AA, 17247 MW, 4E792CB55PF91760 CRG64;	Qy 81 GCCGDEGLHVCAVLTANITMQLKIPPNRDPHSYVEMTPSQDVLCERCPILETTKAERRK 140 Db 84 GCCNDESLECVPEEEFNNTMQLMRKPHOSQH_IGENFLQINKECOPR-----KK 133 Qy 141 TKGRKRQSKTPQ 152 Db 134 DKARQEKCDDKPR 145
RESULT 15 VEGA_CAVPO ID_VEGA_CAVPO AC_P26617; DT_01-AUG-1992 (Rel. 23, Created) DT_01-AUG-1992 (Rel. 23, Last sequence update) DT_10-OCT-2003 (Rel. 42, Last annotation update) DB_Vascular endothelial growth factor A (VEGF-A) (Vascular permeability factor) (VPF). GN_VEGF OR VEGFA. OS_Cavia porcellus (Guinea pig). OC_Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia. OC_NCBITAXID=10141; RN_RPSEQUENCE FROM N.A. RC_TISSUE-Bile duct; RA_Barse B.; RL_Submitted (JAN-1992) to the EMBL/GenBank/DBJ databases. CC_FUNCTION: Growth factor active in angiogenesis, and endothelial cell growth. Induces endothelial proliferation and vascular permeability (By similarity). CC_SUBUNIT: Homodimer; disulfide-linked. Also found as heterodimer with PIGF (By similarity). CC_SUBCELLULAR_LOCATION: Secreted but remains associated to cells or to the extracellular matrix unless released by heparin (By similarity). CC_SIMILARITY: Belongs to the PDGF/VEGF growth factor family. CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch). CC DR_M84230; AAA37057; 1; CC DR_HSSP; P15692; 1VGH. CC DR_InterPro; IPR000400; GP_cysknot. CC DR_ProDom; PD001629; PD_growth_factor; 1. CC DR_Pfam; PF00341; PDGF; 1. CC DR_PRINTS; PR00438; GFCKYSKNOT. CC DR_ProDom; PD001629; PD_growth_factor; 1. CC DR_SM00141; PDGF; 1. CC DR_PROSITE; PS50278; PDGF; 2; 1. CC DR_Mitogen; Angiogenesis; Growth factor; Glycoprotein; Signal; Heparin-binding; Multigene family. CC FT_CHAIN 27 146 BY SIMILARITY. CC FT_DISULFID 51 93 BY SIMILARITY. CC FT_DISULFID 82 127 BY SIMILARITY. CC FT_DISULFID 86 129 BY SIMILARITY. CC FT_DISULFID 76 76 INTERCHAIN (BY SIMILARITY). CC FT_DISULFID 85 85 INTERCHAIN (BY SIMILARITY). CC FT_CARBONYD 100 100 N-LINKED (GLCNAC. . .) (POTENTIAL). CC SQ_SEQUENCE 146 AA, 19330 MW, 9EBB6A81A9D5DCA4 CRC64;	Qy 81 GCCGDEGLHVCAVLTANITMQLKIPPNRDPHSYVEMTPSQDVLCERCPILETTKAERRK 140 Db 84 GCCNDESLECVPEEEFNNTMQLMRKPHOSQH_IGENFLQINKECOPR-----KK 133 Qy 141 TKGRKRQSKTPQ 152 Db 134 DKARQEKCDDKPR 145
Query Match 33.3%; Score 282; DB 1; Length 146; Best Local Similarity 43.9%; Pred. No. 2.7e-22; Matches 58; Conservative 20; Mismatches 44; Indels 10; Gaps 2; Qy 21 SQGALSAGNNSTEMEVYVPENEYWGRGSYCRPMKLUVIADEHPNEVSHIEFSPSCULLSRCS 80 Db 24 SQAAPMAEGGQKRPHEVNKFMDYQRSRSPRPIETLVDFQEXPDELETEFIFKPSVCVPLMRCCG 83	Query Match 33.2%; Score 280.5; DB 1; Length 164; Best Local Similarity 50.0%; Pred. No. 4.4e-22; Matches 57; Conservative 15; Mismatches 33; Indels 9; Gaps 2; Qy 35 EVVPFDVWGRGSYCRPMKLUVIADEHPNEVSHIEFSPSCULLSRCS 94 Db 12 EEVKFMNDVYKRSYCRPIELMVDIFQEXPDELETEFIFKPSVCVPLMRCCGNDSELCYPT 71

Qy 95 TANITMQILKIPPNRDPHSYVENTFSQDVLCERPILETTK-----AERRK 140
| | | | | | : | | | | | | | | | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 72 EFNITMQIMRKPHQOH-I GENSFLQHSKCECRPKKEKAQENPCGPSCSERK 124
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Search completed: September 13, 2004, 09:51:24
Job time : 24 secs

Light

Dark

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: September 13, 2004, 09:44:09 ; search time 116 Seconds

Perfect score: 846
Sequence: 1 MLANKLFTCFLQVLAGLAVH.....RKTGKRXQSXTPTPEPHL 158
Scoring table: BLOSUM62
Gapop 10.0 , Gapext: 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing First 45 summaries

Database :

SPTREMBL 25:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_invertebrate:*
- 5: sp_human:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rabbit:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_xvirus:*
- 16: sp_bacterioplasm:*
- 17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	322.5	38.1	108	6 Q8HY75	Q8hy75 orvis arries
2	300	35.5	189	6 Q95LQ4	Q95lq4 felis silvile
3	299.5	35.4	190	11 Q91ZB1	Q91zb1 rattus norvegicus
4	295.5	34.9	184	6 Q8HY70	Q8hy70 mustela vison
5	295	34.9	191	4 Q96KJ0	Q96kj0 homo sapiens
6	295	34.9	191	4 Q96LB2	Q96lb2 homo sapiens
7	295	34.9	191	6 Q95NE5	Q95ne5 macaca fasciata
8	294.5	34.8	190	11 Q9QX39	Q9qx39 spelax leucopus
9	290	34.3	126	6 Q9BDP7	Q9bdp7 macaca mulatta
10	288.5	34.1	124	6 Q8SPZ9	Q8spz9 sus scrofa
11	288.5	34.1	128	6 Q8SPFL5	Q8spfl5 equus caballus
12	287.5	34.0	127	6 Q8BMO4	Q8bmo4 equus caballus
13	280.5	33.2	190	6 Q77643	Q77643 ovis arries
14	278	32.9	120	6 Q86G64	Q86g64 orctolagus cuniculus
15	276.5	32.7	144	13 Q73822	Q73822 brachydanio
16	275	32.5	118	6 Q9MZB1	Q9mzb1 ovis arries

SEQUENCE FROM N.A.
RP TISSUE=Placenta;
RC MEDLINE=2.1946003; PubMed=11945079;

RX RA

AC DR

ID DT

Q8HY75; AC DT

(TREMBLrel. 23, Created)

01-MAR-2003 (TREMBLrel. 23, Last sequence update)

01-OCT-2003 (TREMBLrel. 25, Last annotation update)

DB DB

Placental Growth Factor (Fragment).

OS OS

Ovis arries (Sheep).

OC OC

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

OC OC

Bovidae; Caprinae; Ovis.

NCBI_TAXID=9940; OX

RN [1]

RN

RP SEQUENCE FROM N.A.

RC TISSUE=Placenta;

RX MEDLINE=2.1946003; PubMed=11945079;

RA RA

Regnauld T.R.H., Orbus R.J., de Vrijer B., Daviden M.L., Galan H.L., Wilkening R.B., Anthony R.V.

RT RT

"Placental expression of VEGF, PIGF and their receptors in a model of Placental insufficiency-intrauterine growth restriction (PI-TUGR).";

RL RL

Placenta 23:132-144 (2002).

EMBL_AY157708; AAN77495.1; -

DR DR

GO; GO:0016020; C:membrane; IEA.

DR DR

GO; GO:0008083; F:growth factor activity; IEA.

DR DR

Wilkening R.B., Anthony R.V.

RT RT

"Placental expression of VEGF, PIGF and their receptors in a model of

Placental insufficiency-intrauterine growth restriction (PI-TUGR).";

DR DR

Prodom; PD001659; PD:growth_factor; 1.

DR DR

SMART, SM00141; PDGF; 1.

DR DR

PROSTE; PS00249; PDGF; 1.

DR DR

INTERPRO; IPR000072; PD_growth_factor.

DR DR

Pfam; PF00341; PDGF; 1.

ProDom; PD001659; PD:growth_factor; 1.

DR DR

GO; GO:0016020; C:membrane; IEA.

DR DR

GO; GO:0008083; F:growth factor activity; IEA.

DR DR

Wilkening R.B., Anthony R.V.

RT RT

"Placental expression of VEGF, PIGF and their receptors in a model of

Placental insufficiency-intrauterine growth restriction (PI-TUGR).";

RL RL

Placenta 23:132-144 (2002).

EMBL_AY157708; AAN77495.1; -

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GO; GO:0016020; C:membrane; IEA.

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GO; GO:0008083; F:growth factor activity; IEA.

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Placenta 23:132-144 (2002).

EMBL_AY157708; AAN77495.1; -

DR DR

GO; GO:0016020; C:membrane; IEA.

DR DR

GO; GO:0008083; F:growth factor activity; IEA.

DR DR

Wilkening R.B., Anthony R.V.

RT RT

NCBI_TAXID:9685;
 RN [1] _
 RP SEQUENCE FROM N.A.
 RA Koga L., Kobayashi Y., Yazawa M., Masuda K., Ohno K., Tsujimoto H.;
 RA "Nucleotide sequence and expression of the feline vascular endothelial
 RT Growth Factor.";
 RT Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
 RL EMBL; AB071947; BMBB0520.1; ~.
 DR GO; GO:0016020; C:membrane; IBA.
 DR GO; GO:0008083; F:growth factor activity; IEA.
 DR GO; GO:0008151; P:cell growth and/or maintenance; IEA.
 DR InterPro; IPR002400; GE_cysknot.
 DR InterPro; IPR00072; PD_growth_factor.

DR PRINTS; PRO00438; GFCKSYKNOT.
DR PRODOM; PDD001629; PD growth factor: 1.

26 *SEQUENCE*, 189 AA; 22193 MW; C1E446759AB3FD6 CRC64;

Query	Match	Best Local Similarity	Score	DB	Length	Capo
Matches	63;	Conservative	49.6%;	Pred.	No. 1-26;	
				Mismatches	41:	Indels

24 SQAAPMADGEHKPHEVYKFMDDVYQRSYCRPIETLVDFQEYDEIEYIFKPSCVPLMRCG 83
Db

Qy	81	GCGDEGLCYALKTANTMQLI KIPPNRDPSVYEMTESQDVLCERPLETTK----	131
D _b	84	GCCNDREGFCYDPTERENTMOTMPLKPPGCGC TCRMSPYQHCKPQVWVDDC	144

136 -AERRK 140
QY

Db 143 PCSERRK 149

RESULT 3

~~SECRET~~
ID Q91ZE1
AC Q91ZE1;
PRELIMINARY;
PRT; 190 AA.

DT 01-DEC-2001 (TREMBUREL. 19, Created)
 DT 01-DEC-2001 (TREMBUREL. 19, Last sequence update)
 DDT 01-JUN-2003 (TREMBUREL. 24, Last annotation update)

DE Vascular endothelial growth factor.
GDNF
VEGF.

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OC *Rattus norvegicus* (L.)

NCBI_TaxID=10116;
OX [1]
RN SEQUENCE FROM N_A.
RP

	Matches	Conservative	Mismatches	Indels	Gaps	2;
Y	21	SQGAGNSTMEEVPPNEWGRSGRPMEXKLYTADEHPNEVSHIFSPSCVLLSRCS	80			
b	24	SQAAPMAEGEHKPHHEVKEMDVQSYCRPIELVLDI				83
Y	81	GCCGDEGLHCVALKTANITMQLKPPNDRPHSYEMTFSQDVLCECRPILETTK----	135			
b	84	GCCNDEGLECPTEENITMQLMRPHQH-IGEMSFLQHNRCERPKDKDARQENPC	142			
	136	--AERRK 140				
Y	143	GPCSERRK 150				
		RESULT 5				
C	Q96K00	PRELIMINARY;				
C	Q96K10	PRT; 191 AA.				
T	01-DEC-2001	(TREMBLrel. 19, Created)				
T	01-JUN-2003	(TREMBLrel. 24, Last annotation update)				
E	Vascular endothelial growth factor 165b.					
E	Homo sapiens (Human).					
S	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
S	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
X	[NCBI_TaxID=96676; NCBI_N[1]]					
P	SEQUENCE FROM N.A.					
C	TISSUE=Kidney.					
C	Sugino M., Winkler M., Gillatt D., Harper S.J., Bates D.O.;					
C	"A new isoform of vascular endothelial growth factor mRNA is down-regulated in renal tumors.";					
L	(In) Unknown A. (eds.);					
L	Proceedings of the 7th World Congress on Microcirculation, pp.3-3,					
L	Sydney, Australia (2001).					
R	EMBL: AF310806; AAU27435; 1.					
R	GO: 0016020; C membrane IEA.					
R	GO: 0008083; F: growth factor activity; IEA.					
R	GO: 0008115; P: cell growth and/or maintenance; IEA.					
R	Inter-Pro: IPR02400; GF_cysknob.					
R	Intertier_1; IPR00072; PD_growth_factor.					
R	PFam: PF00341; PDGF_1.					
R	PRINTS: PR00438; GFCKYSKNOT.					
R	PRODOM: PD001629; PD_growth_factor_1.					
R	SMART: SM00141; PDGF_1.					
R	PROSITE: PS00249; PDGF_1;					
R	PROSITE; PS50278; PDGF_2;					
Q	SEQUENCE 191 AA; 22258 MW; D25243E540AC79BD CRC64?					
	Query Match Score 34.9%;	Score 295;	DB 4;	Length 191;		
	Best Local Similarity 47.3%;	Pred. No. 4.1e-26;				
Matches	61; Conservative	Mismatches 19;	Indels 39;	Gaps 10;	Gaps 3;	
Dy	21	SQGA-LSAGNNSTMEEVPPNEWGRSGRPMEXKLYTADEHPNEVSHIFSPSCVLLSRCS	79			
Db	24	SQAAPMAEGEHKPHHEVKEMDVQSYCRPIELVLDI				83
Dy	80	SGCCGDEGLHCVALKTANITMQLKPPNDRPHSYEMTFSQDVLCECRPILETTK----	135			
Db	84	GGCNDGSLECPTEENITMQLMRPHQH-IGEMSFLQHNRCERPKDKDARQENPC	142			
Dy	136	--AERRK 140				
Db	143	CGPSEERRK 151				
		RESULT 6				
	296L82	PRELIMINARY;				
	Q96L82	PRT; 191 AA.				
	Q96L82;					
	01-DEC-2001	(TREMBLrel. 19, Created)				
	01-DEC-2001	(TREMBLrel. 19, Last sequence update)				

DR	GO:0016020; C:membrane; IEA.	QY	61 HPMEVSHIFSPSCVLLSRSGCCGDEGLHCVALLTANITMQLKIPPNRDPHSYVEMTFS 120
DR	GO:0008033; F:growth factor activity; IEA.	DR	64 YPDELEYIKPSCPPLMRGGCCNDDEAECVPTESNTMQIMIKPHQSQH-IGEMSEI_122
DR	GO:0008151; P:cell growth and/or maintenance; IEA.	Db	121 QDVLCRCPPILETK-----AERK 140
DR	InterPro; IPR002400; GF_cysknot.	QY	123 QHNRCCECRPKDKDRLHENHCEPCSERK 150
Pfam;	PF000341; PDGF_1.	Db	
PRINTS;	PR00438; GFCYSKNOT.		
ProDom;	PD001629; PD_growth_factor; 1.		
DR	PROSITE; PS00249; PDGF_1; 1.		
DR	PROSITE; PS50378; PDGF_2; 1.		
SQ	SEQUENCE 191 AA; 22314 MW; CCE57097DD3779BD CRC64;		
		RESULT 9	
		ID Q9BDP7	PRELIMINARY; PRT; 126 AA.
		AC Q9BDP7;	
		DT 01-JUN-2001 (TrEMBLrel. 17, Created)	
		DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)	
		DB 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)	
		DB Vascular endothelial growth factor (fragment).	
		OS Macaca mulatta (Rhesus macaque).	
		OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
		OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;	
		OC Cercopithecinae; Macacidae.	
		OX NCBI_TaxID=9544;	
		RN [1]	
		RP SEQUENCE FROM N.A.	
		RA RA Hazard T.M., Nayak N.R., Jia Y., Strouffer R.L.;	
		RT "Rhesus macaque VEGF mRNA sequence."	
		RL Submitted (JAN-2001) to the EMBL/Genbank/DBJ/ databases.	
		DR EML; AF339737; AAK26379.1; -.	
		DR HSSP; P49763; 1FZV.	
		DR GO; GO:0116030; C:membrane; IEA.	
		DR GO; GO:0008083; F:growth factor activity; IEA.	
		DR InterPro; IPR002400; GF_cytknot.	
		DR Pfam; PF00341; PDGF_1.	
		DR PRINTS; PR00438; GFCYSKNOT.	
		DR ProDom; PD001629; PD_growth_factor; 1.	
		DR SMART; SM00141; PDGF_1.	
		DR PROSITE; PS00249; PDGF_1; 1.	
		DR PROSITE; PS50378; PDGF_2; 1.	
		FT NON-TER 1 126 126	
		FT SEQENCE 126 AA; 14599 MW; 1175F2386A883BCF CRC64;	
		Query Match 34.3%; Score 290; DB 6; Length 126;	
		Best Local Similarity 51.8%; Pred. No. 9.5e-26;	
		Matches 57; Conservative 16; Mismatches 35; Indels 2; Gaps 2;	
		RESULT 8	
		ID Q9QX39	PRELIMINARY; PRT; 190 AA.
		AC Q9QX39;	
		DT 01-MAY-2000 (TrEMBLrel. 13, Created)	
		DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)	
		DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)	
		DE Vascular endothelial growth factor.	
		GN VEGF.	
		OS Spalax leucodon ehrenbergi (Ehrenberg's mole rat).	
		OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;	
		OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Spalacinae;	
		OC Nannospalax.	
		NCBI_TaxID=30637;	
		RN [1]	
		RP SEQUENCE FROM N.A.	
		RA Avivi A., Resnick M.B., Nevo E., Joel A., Levy A.P.;	
		RT "Adaptive hypoxic tolerance in the subterranean mole rat Spalax ehrenbergi: the role of vascular endothelial growth factor.";	
		RL PEBS Lett. 452:133-140(1999).	
		DR EML; AF186236; AAD56245.1; -.	
		DR HSSP; P49763; 1FZV.	
		DR GO; GO:0016020; C:membrane; IEA.	
		DR GO; GO:0008083; F:growth factor activity; IEA.	
		DR GO; GO:0008151; P:cell growth and/or maintenance; IEA.	
		DR InterPro; IPR002400; GF_cysknot.	
		DR InterPro; IPR000072; PD_growth_factor.	
		DR Pfam; PR00341; PDGF_1.	
		DR PROSITE; PR00438; GFCYSKNOT.	
		DR ProDom; PD001629; PD_growth_factor; 1.	
		DR SMART; SM00141; PDGF_1.	
		DR PROSITE; PS00249; PDGF_1.	
		DR PROSITE; PS50378; PDGF_2; 1.	
SQ	SEQUENCE 190 AA; 22488 MW; 2228383BC65F0BEE CRC64;		
		Query Match 34.8%; Score 294.5; DB 11; Length 190;	
		Best Local Similarity 43.9%; Pred. No. 4.6e-26;	
		Matches 65; Conservative 21; Mismatches 53; Indels 9; Gaps 2;	
		RESULT 10	
		ID Q8SPZ9	PRELIMINARY; PRT; 124 AA.
		AC Q8SPZ9;	
		DT 01-JUN-2002 (TrEMBLrel. 21, Created)	
		DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)	
		DB Vascular endothelial growth factor (fragment).	
		OS Sus scrofa (Pig).	
		OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
		OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.	
		NCBI_TaxID=9823;	
		RN [1]	
		RP SEQUENCE FROM N.A.	
		RC TISUE=Myocardium;	
		RC Yuan H., Li J.;	

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 13, 2004, 09:45:39 ; Search time 39 Seconds
 (389,699 million cell updates/sec)

Title: US-10-071-370A-4
 Perfect score: 846
 Sequence: 1 MILAMKLFTCFLQVLAGLAVH.....RKTGKGRKQSKTPQTEPEBLH 158

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues
 Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing First 45 summaries

Database : PIR_78;*
 1: Pir1;*
 2: Pir2;*
 3: Pir3;*
 4: Pir4;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	846	100.0	158	2 A56125	placental growth f
2	474.5	56.1	149	2 A1236	placental growth f
3	320.5	37.9	214	2 A44881	vascular endotheli
4	315	37.2	232	2 A41551	vascular endotheli
5	300.5	35.5	190	2 B44881	vascular endotheli
6	299.5	35.4	190	2 A35987	glioma-derived vas
7	295	35.0	190	2 S55130	vascular endotheli
8	283.5	33.5	190	2 B40080	ovine vascular end
9	282	33.3	146	2 S57956	vascular endotheli
10	278	32.9	120	2 A33787	vascular endotheli
11	233	27.5	128	2 151295	vascular endotheli
12	193	22.8	133	2 B49330	vascular endotheli
13	188	22.2	207	2 JC4579	vascular endotheli
14	184	21.7	188	2 D49530	16K vascular endo
15	167	19.7	148	2 S69207	vascular endotheli
16	144	17.0	419	2 S25097	platelet-derived g
17	114	13.5	225	1 PFMGB	platelet-derived g
18	112	13.2	241	1 TUCSS	platelet-derived g
19	110	13.0	245	1 PFHUG2	platelet-derived g
20	108	12.8	241	1 TVMYS9	PDGF-related trans
21	96.5	11.4	226	1 A25669	platelet-derived g
22	96.5	11.4	271	2 S25096	platelet-derived g
23	92.5	10.9	197	2 151550	platelet-derived g
24	89.5	10.6	211	1 JC7592	platelet-derived g
25	84.5	10.6	215	2 A48851	platelet-derived g
26	84.5	10.0	196	2 151550	spinal cord derive
27	83	9.8	226	2 JC7592	platelet-derived g
28	82.5	9.8	370	2 JC7998	spinal cord derive
29	82	9.7	370	2 JC7998	platelet-derived g

RESULT 1

A56125

placental growth factor precursor - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 19-Oct-1995 #sequence_revision 19-Oct-1995 #text_change 05-Nov-1999

C:Accession: A56125

R. DiSalvo, J.; Bayne, M.L.; Conn, G.; Kwolek, P.W.; Trivedi, P.G.; Soderman, D.D.; Palisi,

J. Biol. Chem. 270, 7717-7723, 1995

A:Title: Purification and characterization of a naturally occurring vascular endothelial

A:Reference number: A56125; PMID:7706320

A:Accession: A56125

A:Status: preliminary; not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-158 <DIS>

A:Cross-references: GB:IA40030; PIDN:AAA97425.1; PIDN:AAA97425.1; PID:91263414

C:Keywords: glycoprotein

Query Match 100.0%; Score 846; DB 2; Length 158;

Best Local Similarity 100.0%; Pred. NO. 4.4E-78;

Matches 158; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query 1 MLMAMKFTCPLQVLAGLAVSQGALSAGNISTEMEVYPENWGRSYCRPMEKLYIADE 60

Db 1 MLMAMKFTCPLQVLAGLAVSQGALSAGNISTEMEVYPENWGRSYCRPMEKLYIADE 60

Query 61 HPNEVSHIFSPSCVLISRCSSCGDGLCVALKTANITMQILKIPNRPDHSYVNTFS 120

Db 61 HPNEVSHIFSPSCVLISRCSSCGDGLCVALKTANITMQILKIPNRPDHSYVNTFS 120

Query 121 QDVLCBRCRPILETTKAERRRTKGKRSKTPQTEBHL 158

Db 121 QDVLCBRCRPILETTKAERRRTKGKRSKTPQTEBHL 158

RESULT 2

A41236

placental growth factor precursor - human

C:Species: Homo sapiens (man)

C:Date: 19-Jun-1992 #sequence_revision 19-Jun-1992 #text_change 05-Jun-1999

C:Accession: A41236

C:Maglione, D.; Guerrriero, V.; Viglietto, G.; Dell'i-Bovi, P.; Persico, M.G.

R.Maglione, D.; Guerrriero, V.; Viglietto, G.; Dell'i-Bovi, P.; Persico, M.G.

Proc. Natl. Acad. Sci. U.S.A. 88, 9267-9271, 1991

A:Title: Isolation of a human placenta cDNA coding for a protein related to the vascular

A:Reference number: A41236; PMID:92021031; PMID:124389

A:Accession: A41236

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-149 <MAG>

A:Cross-references: GB:X54936; NID:935521

C:Genetics:

A:Gene: PGF

A:Cross-references: GDB:134676; OMIM:601121

ALIGNMENTS

A; Map Position: 14q24-14q31	Query Match 56.1%; Score 474.5%; DB 2; Length 149;	Qy 141 TKGKRKOSK 149
Best Local Similarity 64.1%; Pred. No. 1.4e-40;	Db 143 VRGKGKQK 151	
Matches 91; Conservative 19; Mismatches 27; Indels 5; Gaps 2;		
		RESULT 4
QY 1 MLAMKLFTCFQVLLAGLAVHS---QGALSAGNNSTEMEVYPFNEYWGRGSYCRPMELKYY 56	A41551	
Db 1 MPVMLRLFCPFQQLLAGLALLAVPPQWALSGNGSSEVEVTPFQETWGRSYCRALERLVD 60		vascular endothelial growth factor 206 precursor - human
QY 57 IADEHFNVEYSHIFSPSCVLLSRCSGCCGDEGLHCTALKTANITMQILKIPPNRDPHSIVTE 116	N;Alternate names: vascular permeability factor	
Db 61 VVSEPTSEVHMFSQSCVLLSLRCCGDENLHCVPETANTVMQLLKTRSGDRP-SYVE 119	N;Contains: Homo sapiens (man)	
QY 117 MTFSDQVLCRCPRLFTKAER 138	C;Species: Homo sapiens (man)	
Db 120 LTFSDQHVRCECRCPRLREKPER 141	C;Date: 28-Aug-1992 #sequence revision 28-Aug-1992 #text_change 05-Nov-1999	
	C;Accession: A41551; C41551; B41551; A40454; C40454; A40080; JQ1463; D.W.	
	R;Houck, K.A.; Ferrara, N.; Winer, J.; Cachianes, G.; Li, B.; Leung, D.W.	
	Mol. Endocrinol. 5, 1806-1814, 1991	
	A;Title: The vascular endothelial growth factor family: identification of a fourth mole	
	A;Reference number: A41551; MUID:32168017; PMID:1791831	
	A;Accession: A41551;	
	A;Molecule type: mRNA	
	A;Residues: 1-232 <HOU1>	
	A;Cross-references: GB:885192; NID:g246155; PID:9246156	
	A;Accession: C41551	
	A;Species: nucleic acid sequence not shown	
	A;Molecule type: tRNA	
	A;Accessories: 1-140, 'N', 183-232 <HOU2>	
	A;Accession: B41551	
	A;Species: nucleic acid sequence not shown; not compared with conceptual translation	
	A;Molecule type: mRNA	
	A;Accessories: 1-141,227-232 <HOU>	
	R;Tischer, E.; Mitchell, R.; Hartman, T.; Silva, M.; Gospodarowicz, D.; Fiddes, J.C.; Al-J. Biol. Chem. 266, 11947-11954, 1991	
	A;Title: The human gene for vascular endothelial growth factor. Multiple protein forms as A;Reference number: A40454; MUID:91268072; PMID:1711045	
	A;Accession: A40454	
	A;Molecule type: DNA	
	A;Accessories: 1-165,183-232 <TI1>	
	A;Cross-references: GB: M63971; GB:M63972; GB:M63973; GB:M63974; GB:M63975; GB:	
	A;Accession: B40454	
	A;Molecule type: DNA	
	A;Accessories: 1-141,227-232 <TI3>	
	A;Cross-references: GB: M63971; GB:M63972; GB:M63974; GB:M63975; GB:M63978	
	A;Accession: C40454	
	A;Molecule type: DNA	
	A;Accessories: 1-140, 'N', 183-232 <TI2>	
	A;Cross-references: GB: M63971; GB:M63972; GB:M63973; GB:M63974; GB:M63975; GB:	
	A;Accessories: 1-140, 1309-1312, 1989	
	A;Title: Vascular permeability factor, an endothelial cell mitogen related to PDGF.	
	A;Reference number: A40079; MUID:906960; PMID:2479987	
	A;Accession: A40079	
	A;Species: not compared with conceptual translation	
	A;Molecule type: mRNA	
	A;Accessories: 1-165,183-232 <KBC>	
	A;Cross-references: GB: M27281; NID:9340300; PIDN:AAA36807.1; PID:934031	
	R;Leung, D.W.; Cachianes, G.; Kuang, W.J.; Goeddel, D.V.; Ferrara, N.	
	Science 246, 1306-1309, 1989	
	R;Weinberg, K.; Marne, D.; Welch, H.A.	
	Biochem. Biophys. Res. Commun. 183, 1167-1174, 1992	
	A;Title: Vascular endothelial growth factor is a secreted angiogenic mitogen.	
	A;Reference number: A40080; MUID:9069608; PMID:2479986	
	A;Accession: A40080	
	A;Species: not compared with conceptual translation	
	A;Molecule type: mRNA	
	A;Accessories: 1-140, 'N', 183-232 <LEU>	
	A;Cross-references: GB: M32972; NID:9181970; PIDN:AAA35789.1; PID:9181971	
	R;Weinberg, K.; Marne, D.; Welch, H.A.	
	Biochem. Biophys. Res. Commun. 183, 1167-1174, 1992	
	A;Title: AIDS-associated Kaposi's sarcoma cells in culture express vascular endothelial s	
	A;Reference number: JQ1463; MUID:92231879; PMID:1567395	
	A;Accession: JQ1463	
	Query Match 37.9%; Score 320.5%; DB 2; Length 214;	
Best Local Similarity 48.1%; Pred. No. 7.5e-25;		
Matches 62; Conservative 20; Mismatches 46; Indels 1; Gaps 1;		
	RESULT 3	
QY 21 SQGLISAGNNSTEMEVYPFNEYWGRGSYCRPMELKYYADEHPNEWVSHIFSPSCVLLSRCS 80		
Db 24 SQQAQTTEGEQSKSHEVKFMDVYQRSYCYCPDIELTYFLDIFYPDIEYFKPSYCLMRCA 83		
QY 81 GCCCDDEGLICVALKTANITMQILKIPPNRDPHSIVTEMPSQDWLCECRPILETTKAERK 140		
Db 84 GGCNDEALECVPTPSBSNTMQMKPHQSQH-IGEMSLQHCSRCECPKKDKTPKEPKS 142		
	A;Cross-references: EMBL:X65568; NID:937658; PID:CAA4447.1; PMID:937659	
	A;Experimental source: AIDS-Kaposi's sarcoma cell	
	A;Accession: JQ1463	

A; Molecule type: mRNA
A; Residues: 1-140, 'N', 227-232 <WE2>
A; Experimental source: AIDS-Kaposi's sarcoma cell line; Nelson, R.; Siegel, N.; Hay
R; Connolly, D.T.; Olander, J.V.; Heuvelman, D.; Nelson, R.; Siegel, N.; Siegel, N.;
J. Biol. Chem. 264, 20017-20024, 1989
A; Title: Human vascular permeability factor. Isolation from U937 cells.
A; Reference number: A34492; MUID:90062112; PMID:2584205
A; Accession: A34492
A; Molecule type: protein
A; Residues: 27-36; 43-49, 'R'; 72-76, 'Q'; 78-81; 59-71 <CON>
C; Comment: The most common of several alternatively spliced forms is VEGF 165.
C; Genetics:
A; Gene: GDB:VEGF
A; Cross-references: GDB:132244; OMIM:192240
A; Map position: 6p21-6p12
C; Function:
A; Description: promotes fluid and protein leakage from blood vessels
C; Keywords: alternative splicing; angiogenesis; dimer; disulfide bond; extracellular pro-
F:1-232/Product: vascular endothelial growth factor 266 precursor #status predicted <V20
F:1-165,183-232/Product: vascular endothelial growth factor 189 precursor #status predicted
F:1-141-227-232/Product: vascular endothelial growth factor 121 precursor #status predicted
F:1-26/Domain: signal sequence #status predicted <SIG>
F:101/Binding site: carbohydrate (Asn) (covalent) #status predicted
Query Match 37.2%; Score 315; DB 2; Length 232;
Best Local Similarity 47.7%; Pred. No. 2.9e-24;
Matches 62; Conservative 21; Mismatches 45; Indels 2; Gaps 2;
Db 21 SQGAGNNSTEMEVPPFNEYWGRSYCRPMEKLVIADEHPNEVSHIFSPCVLILSRCS 79
Db 24 SQAAPMABEGQNHEVVKMDVYQRSYCRPIETLVDIFQEPDIEYIFKPKSCVPLMRC 83
Qy 80 SGCGDDEGLHCVALKTANITMQLIKIPPNPDPHSYVEMTSQDVILECRPILETKAERR 139
Db 84 GGCNCNDEGLECPVTEESNTMQIMRIKPHQGQH-IGEMSFLQHNKCERCPKDARQERK 142
Qy 140 KTKGKRKSK 149
Db 143 SVRGKGK 152

RESULT 5
B44881
vascular endothelial growth factor-1 precursor - mouse
C; Date: 03-Feb-1994 #sequence revision 03-Feb-1994 #text_change 05-Nov-1999
C; Accession: BA44881; A43151; A61029
R; Breier, G.; Albrecht, U.; Sterrer, S.; Rissau, W.
Development 114, 521-532, 1992
A; Title: Expression of vascular endothelial growth factor during embryonic angiogenesis
A; Reference number: A44881; MUID:92274803; PMID:1592003
A; Accession: B44881
A; Molecule type: mRNA
A; Residues: 1-150 <BRE>
A; Cross-references: GB:S38083; PID:9249858; PID:AAB22253.1; PID:9249859
A; Experimental source: embryo
A; Note: sequence extracted from NCBI backbone (NCBIN:107622, NCBIPI:107623)
R; Claffey, K.P.; Wilkison, W.O.; Spiegelman, B.M.
J. Biol. Chem. 267, 16317-16322, 1992
A; Title: Vascular endothelial growth factor. Regulation by cell differentiation and acti-
A; Reference number: A43351; MUID:9235593; PMID:1644816
A; Accession: A43351
A; Molecule type: mRNA
A; Residues: 1-116, 'ER', 119-190 <CLs>
A; Cross-references: GB:M9520; PID:9202350; PID:AAA40547.1; PID:9202351
A; Note: sequence extracted from NCBI backbone (NCBIN:110665, NCBIPI:110675)
R; Rosenthal, R.A.; Megyesi, J.F.; Henzel, W.J.; Ferrara, N.; Folkman, J.
Growth Factors 4, 53-59, 1990
A; Title: Conditioned medium from mouse sarcoma 180 cells contains vascular endothelial growth factors
A; Reference number: A61029; MUID:91197543; PMID:208541
A; Accession: A61029
A; Molecule type: protein
A; Residues: 27-38 <ROS>

C; Keywords: alternative splicing; angiogenesis; dimer; disulfide bond; glycoprotein; mito-
Query Match 35.5%; Score 300.5; DB 2; Length 190;
Best Local Similarity 47.7%; Pred. No. 6.9e-23; Indels 9; Gaps 2;
Matches 61; Conservative 18; Mismatches 40;
Qy 21 SQGAGNNSTEMEVPPFNEYWGRSYCRPMEKLVIADEHPNEVSHIFSPCVLILSRCS 80
Db 24 SQAAPMABEGQNHEVVKMDVYQRSYCRPIETLVDIFQEPDIEYIFKPKSCVPLMRC 83
Qy 81 GGCGDDEGLHCVALKTANITMQLIKIPPNPDPHSYVEMTSQDVILECRPILETTK---- 135
Db 84 GCCNDALECPVTEESNTMQIMRIKPHQGQH-IGEMSFLQHNKCERCPKDRTKPPENHC 142
Qy 136 --AERK 140
Db 143 EPCSRERK 150

RESULT 6
A5987
Gioma-derived vascular endothelial cell growth factor - rat
C; Species: Rattus norvegicus (Norway rat)
C; Date: 16-Nov-1990 #sequence_revision 16-Nov-1990 #text_change 05-Nov-1999
C; Accession: A35987
R; Conn, G.; Bayne, M.L.; Soderman, D.D.; Kwok, P.W.; Sullivan, K.A.; Palisi, T.M.; Hope,
Proc. Natl. Acad. Sci. U.S.A. 87, 2628-2632, 1990
A; Title: Amino acid and cDNA sequences of a vascular endothelial cell mitogen that is homologous to the vascular endothelial growth factor - rat
A; Accession: A35987
A; Cross-references: GB:M32167; NID:9204287; PID:AAA41211.1; PMID:9204288
A; Molecule type: mRNA
A; Residues: 1-190 <CON>
A; Cross-references: GB:M32167; NID:9204287; PID:AAA41211.1; PMID:9204288
Query Match 35.4%; Score 299.5; DB 2; Length 190;
Best Local Similarity 47.7%; Pred. No. 8.7e-23; Mismatches 40; Indels 9; Gaps 2;
Matches 61; Conservative 18; Mismatches 40; PMID:2320579
Qy 21 SQGAGNNSTEMEVPPFNEYWGRSYCRPMEKLVIADEHPNEVSHIFSPCVLILSRCS 80
Db 24 SQAAPMABEGQNHEVVKMDVYQRSYCRPIETLVDIFQEPDIEYIFKPKSCVPLMRC 83
Qy 81 GGCGDDEGLHCVALKTANITMQLIKIPPNPDPHSYVEMTSQDVILECRPILETTK---- 135
Db 84 GCCNDALECPVTEESNTMQIMRIKPHQGQH-IGEMSFLQHNKCERCPKDRTKPPENHC 142
Qy 136 --AERK 140
Db 143 EPCSRERK 150

RESULT 7
S52130
vascular endothelial growth factor - pig
C; Species: Sus scrofa domestica (domestic pig)
C; Date: 14-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 05-Nov-1999
C; Accession: BA57559; A43130
R; Sharma, H.S.; Tang, Z.H.; Gho, B.C.G.; Verdouw, P.D.
Biochim. Biophys. Acta 1260, 235-238, 1995
A; Title: Nucleotide sequence and expression of the porcine vascular endothelial growth factor
A; Reference number: S52130; MUID:95143284; PMID:7841203
A; Accession: S52130
A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-190 <SHR>
A; Cross-references: GB:X81380; NID:9587559; PID:CAA57143.1; PMID:9587560
Query Match 35.0%; Score 296.5; DB 2; Length 190;
Best Local Similarity 48.4%; Pred. No. 1.9e-22; Mismatches 40; Indels 9; Gaps 2;
Matches 62; Conservative 17; Mismatches 40; PMID:7841203
Qy 21 SQGAGNNSTEMEVPPFNEYWGRSYCRPMEKLVIADEHPNEVSHIFSPCVLILSRCS 80

Db 24 SQAAPMPEGDKPHEVKFMDYQRSQCRPIITLVDFQHEYDEIEIFKPSCSVPLMRCG 83
 Qy 81 GCGGDEGLHCVALKTANTIMQLIKIPNDRPHSYVNTFSQDVLCECRPILETTK---- 135
 Db 84 GCCNDSEGLECYPTEEFVITMQLMRIXPHQOH-IGEMSFQFLQHNKCECRPKDKDARQENPC 142
 Qy 136 --AERK 140
 Db 143 GPCSERRK 150

RESULT 8
 B40080
 vascular endothelial growth factor precursor (version 2) - bovine
 C;Species: Bos primigenius taurus (cattle)
 C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 05-Nov-1999
 R;Leung, D.W.; Cachianes, G.; Kuang, W.J.; Goeddel, D.V.; Ferrara, N.
 Science 246, 130-139, 1989
 A;Title: Vascular endothelial growth factor is a secreted angiogenic mitogen.
 A;Reference number: A40080; MUID:90069008; PMID:2479966
 A;Accession: B40080
 A;Molecule type: mRNA
 A;Residues: 1-190 <TIS>
 A;Cross-references: GB:M32976; PID:9163006; PID:AAA30502.1; PID:9163007
 R;Fischer, B.-E.; Gospodarowicz, D.; Mitchell, R.; Silva, M.; Schilling, J.; Lau, K.; Criqui
 Biochem. Biophys. Res. Commun. 165, 1198-1206, 1989
 A;Title: Vascular endothelial growth factor: a new member of the platelet-derived growth
 factor family
 A;Accession: B33787
 A;Reference number: A33787; MUID:90121225; PMID:2610687
 A;Molecule type: mRNA
 A;Residues: 27-190 <TIS>
 A;Cross-references: GB:M31836; PID:9163808; PID:AAA30804.1; PID:9163809
 R;Ferrara, N.; Henzel, W.J.
 Biochem. Biophys. Res. Commun. 151, 851-858, 1989
 A;Title: Pituitary follicular cells secrete a novel heparin-binding growth factor specific
 A;Reference number: A33255; MUID:89286596; PMID:2735925
 A;Accession: A33255
 A;Molecule type: protein
 A;Residues: 27-31 <FER>
 C;Keywords: alternative splicing; glycoprotein
 F1-26/Domain: signal sequence #status predicted <SIG>
 F1-27-190/Product: vascular endothelial growth factor #status predicted <MAT>
 F1-100/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 33.5% Score 283.5; DB 2; Length 190;
 Best Local Similarity 46.9%; Pred. No. 3.6e-21; Mismatches 16; Indels 9; Gaps 2;

Db 21 SQAALSGANNSTEMEVVWGRSYCRPMEKLVIADEHPNEVSHIFSPSCVLLSRCS 80
 Db 24 SQAAPMEEGGQKPKHEVKFMDYQRSQCRPIETLVDFQHEYDEIEIFKPSCSVPLMRCG 83

RESULT 9
 S57956
 ovine vascular endothelial growth factor - sheep
 C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
 C;Accession: S57956
 R;Radmer, D.A.; Dai, Y.; Li, J.; Jones, S.C.; Moor, R.M.
 A;Reference number: S57956
 A;Accession: S57956

Query Match 27.5% Score 233; DB 2; Length 128;
 Best Local Similarity 42.9%; Pred. No. 3e-16; Mismatches 21; Indels 6; Gaps 2;

QY	57	IADEPNFEVSHIFSPSCVYLRSRGCCGDEGLHCVALKTANTIMQLIKPPNRDPHSYVE	116	1	MLAMKLFTCFLQVLAGLAVHSQALSAGNNSTEMEVYVPNEVGRSYCRPEMKLVIADE	60
Db	2	IFOPYPDVEYIFRPSCLVPLMRAGGCCDEGLECPVDPVNTMELARIKPHQSQH-IAH	60	4	LLRRLLIVALLQARTAPVSQ	--EDGPHSIQKKVVPWIDYARATCQPREVVPVPSMS
QY	117	MTPSQDVLCRPILET---TKAERERKTKGKRKOSKTPCTPTEEP	156	61	HPNEVSHIFSPSCVYLRSRGCCGDEGLHCVALKTANTIMQLIKPPNRDPHSYV-	EMTF 119
Db	61	MSFQHSKCDCRPKDKVKNQERKSRSKGKGRKRGKRYKPP	105	60	LMGNVVKOLVPSCVTVQRGGCCPDDGLEYCPTGQHQRVMQILMI--QYPSSQLGEMSL	116
RESULT 12				120	SQDVLCECRPILETTKAERRRKTKGKRKOS--KTPQTEBPH	157
B49530				117	EHHSQCECRP-----KKESAVKPDRAIPH	142
vascular endothelial growth factor homolog A2R, 14.7K - Orf virus						
C;Species:	Orf virus	C;Date:	07-Apr-1994	RESULT 14		
C;Accession:	B49530	C;Accession:	JC4680			
R;Virol.	68	R;Virol.	68			
J;Virol.	84-92	J;Virol.	84-92			
A;Title:	Homologs of vascular endothelial growth factor are encoded by the poxvirus orf	A;Title:	Mus musculus (house mouse)			
A;Reference number:	A49530;	A;Reference number:	NCBI:U43837;			
A;Contents:	N22	A;Contents:	GB:U43837;			
A;Accession:	B49530	A;Accession:	R;Townson, S.; Lagercrantz, J.; Grimmond, S.; Silins, G.; Nordenskjold, M.; Weber, G.;			
A;Status:	preliminary	A;Status:	C;Sequence-revision: 19-Jul-1996 #text_change 05-Nov-1999			
A;Residues:	1-133 <LYT>	A;Residues:	C;Cross-references: GB:U43837; NID:g1314335; PIDN:AAAC52553..1; PID:91314336			
A;Cross-references:	GB:S67520;	A;Cross-references:	C;Comment: This factor is a mitogen, that is selective for endothelial cells, and belongs to the poxvirus orf gene.			
A;Note:	sequence inconsistent with nucleotide translation	A;Note:	A;Text: Characterization of the murine VEGF-related factor gene.			
A;Molecule type:	DNA	A;Molecule type:	A;Reference number: JC4679; MUID:96183052; PMID:8607868			
A;Accession:	B49530	A;Accession:	A;Map position: 137/2			
A;Cross-references:	GB:S67520;	A;Cross-references:	A;Intros: 137/2			
A;Note:	sequence extracted from NCBI backbone (NCBIN:141420, NCBI:P:141425)	A;Note:	F;1-1/Domain: signal sequence #status predicted <SIG>			
Query Match	22. 8%	Score	F;22-188/Product: vascular endothelial growth factor-related factor #status predicted <SIG>			
Best Local Similarity	31.5%	Length	F;22-188/Position: 1-188 <TOW>			
Matches	45;	Indels	A;Cross-references: GB:U43837; NID:g1314335; PIDN:AAAC52553..1; PID:91314336			
Conservative	27;	Gaps	C;Comment: This factor is a mitogen, that is selective for endothelial cells, and belongs to the poxvirus orf gene.			
QY	4	MKLFTCFLQVLAGLAVHSQALSAGNNSTEMEVYVPNEVGRSYCRPEMKLVIADEHN	63	1	MLAMKLFTCFLQVLAGLAVHSQALSAGNNSTEMEVYVPNEVGRSYCRPEMKLVIADE	60
Db	1	MKL---LVGILVAVLH-QTLLNADSNTK---GWSEVLIKSGSECKPRPPVVPSETBHE	51	2	DB:U43837;	119
QY	64	EVSHIFSPSCVYLRSRGCCGDEGLHCVALKTANTIMQLIKPPNRDPHSYVEMTSQDV	123	3	LLRRLLIVALLQARTAPVSQ	--EDGPHSIQKKVVPWIDYARATCQPREVVPVPSMS
Db	52	LTSQRNPVPPCTYLMRGCCNDSELCVPPFEVNVTMELLG-ASGSGSNSGMQRLSFVHEK	110	61	HPNEVSHIFSPSCVYLRSRGCCGDEGLHCVALKTANTIMQLIKPPNRDPHSYV-	EMTF 119
QY	124	LCECRPILETTKAERRRKTKGKRK 146		60	LPDQHVMQILMI--QYPSSQLGEMSL	116
Db	111	KCDCRPFRTTPTRPVRERRR 133		120	SQDVLCECRPILETTKAERRRKTKGKRKOS	148
RESULT 13				117	EHHSQCECRP-----KKES 131	
JC4679						
vascular endothelial growth factor-related factor 186 precursor - mouse						
C;Species:	Mus musculus (house mouse)	C;Species:	Orf virus			
C;Date:	10-May-1996	C;Date:	07-Apr-1994 #sequence_revision 18-Nov-1994 #text_change 08-Oct-1999			
A;Cross-references:	GB:U43836;	A;Cross-references:	C;Accession: D49530			
A;Comment:	This factor is a mitogen, that is selective for endothelial cells, and belongs to the poxvirus orf gene.	A;Comment:	R;Lytle, D.J.; Fraser, K.M.; Fleming, S.B.; Mercer, A.A.; Robinson, A.J.			
A;Genetics:		A;Genetics:	J. Virol. 68, 84-92, 1994			
A;Map position:	19	A;Map position:	A;Title: Homologs of vascular endothelial growth factor are encoded by the poxvirus orf .			
A;Accession:	JC4679	A;Accession:	A;Reference number: A49530; MUID:96183052; PMID:8607868			
A;Molecule type:	mRNA	A;Molecule type:	A;Contents: NZ7			
A;Residues:	1-207 <TOW>	A;Residues:	A;Status: preliminary			
A;Cross-references:	GB:U43836;	A;Cross-references:	A;Molecule type: DNA			
A;Comment:	This factor is a mitogen, that is selective for endothelial cells, and belongs to the poxvirus orf gene.	A;Comment:	A;Residues: 1-148 <LYT>			
A;Keywords:	growth factor	A;Keywords:	A;Cross-references: GB:S67522; NID:9456900; PIDN:AAB29223..1; PID:9456102			
F;1-21/Domain:	signal sequence #status predicted <SIG>	F;1-21/Domain:	A;Note: sequence extracted from NCBI backbone (NCBIN:141422; NCBI:P:141426)			
Query Match	22.2%	Score	Best Local Similarity	33.1%	Length	207;
Matches	53;	Indels	Conservative	22;	Gaps	5;

Query	Match	19.7%	Score	167	DB	2;	Length	148;
Best Local Matches	Similarity	28.1%	Prod. No.	1.6e-09;				
Matches 43;	Conservative	31;	Mismatches	59;	Indels	20;	Gaps	6;
QY	4	MKLFTCPFLQVLAGLAV--HSQGALSAGNNSTEMEVVPEFNEVGR---			-SYCRPMEKLVV	56		
Db	1	MKL-TATLQVVAALLIWMYNLNPCLPCVSQNDSP	--	--	-PTNDMWRTLDKGCKERDTVVY	54		
QY	57	IADEHPNEVSHIFSPSCVYLSSRGCCGDEGLHCVALKTAN--ITMQILKIPPNRDPHSY				114		
Db	55	LGEEYPPESTNLQYNPRCVTKERCGCNGDQCTCAVETRNTTVY					VTVGVSSESGTNSG	114
QY	115	V----EMTFSDQVLCLCPRIELTTAERRTK						
Db	115	VSTNLRQISVTEHTKCDIGRTTTPPTTRPR						147

Search completed: September 13, 2004, 09:54:11
Job time : 40 secs